

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 20:03:45 ; Search time 12448.6 Seconds

(without alignments)
13249.270 Million cell updates/sec

Title: US-09-993-420A-1

Perfect score: 6560

Sequence: 1 atcgatagtcgtcaccacaat.....gtttgtataaaattatcaaa 6560

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues 49582208

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Database :

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: /cgn2_6/ptodata/1/pna/US0506.COMB.seq.*
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Result No.	Score	Query Match	DB Length	ID	Description
1	6541.8	99.7	6560	US-09-993-420A-1	Sequence 1, Appl1
2	6529.8	99.5	6559	US-07-927-661-1	Sequence 1, Appl1
3	6529.8	99.5	6559	US-08-288-295-1	Sequence 1, Appl1
4	6529.8	99.5	6559	US-08-801-248-1	Sequence 1, Appl1
5	713	10.9	713	US-60-360-039-199563	Sequence 29563, A
6	632.6	9.6	1315	US-07-927-661-2	Sequence 2, Appl1
7	632.6	9.6	1315	US-08-288-295-2	Sequence 2, Appl1
8	632.6	9.6	1315	US-08-288-295-4	Sequence 4, Appl1
9	632.6	9.6	1315	US-08-288-295-5	Sequence 4, Appl1
10	632.6	9.6	1315	US-08-288-295-6	Sequence 4, Appl1
11	632.6	9.6	1315	US-08-801-248-2	Sequence 6, Appl1
12	632.6	9.6	1315	US-08-801-248-4	Sequence 2, Appl1
13	632.6	9.6	1315	US-08-801-248-5	Sequence 4, Appl1
14	632.6	9.6	1315	US-08-801-248-6	Sequence 5, Appl1
15	632.6	9.6	1315	US-09-993-420A-2	Sequence 6, Appl1
16	632.6	9.6	1315	US-09-993-420A-4	Sequence 2, Appl1
17	632.6	9.6	1315	US-09-993-420A-5	Sequence 4, Appl1
18	632.6	9.6	1315	US-09-993-420A-6	Sequence 5, Appl1
19	149	2.3	716	US-60-360-039-29178	Sequence 29178, A
20	139.2	2.1	7653	US-07-979-658-18	Sequence 18, Appl1
21	139.2	2.1	7653	US-07-984-182-1	Sequence 1, Appl1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22 139.2 2.1 7653 4 US-08-080-850A-1 Sequence 1, Appli
C 23 139.2 2.1 7653 6 US-08-258-287A-1 Sequence 1, Appli
C 24 139.2 2.1 7653 6 US-08-282-211-1 Sequence 1, Appli
C 25 139.2 2.1 7653 6 US-08-282-211A-1 Sequence 1, Appli
C 26 139.2 2.1 7653 6 US-08-287-669-18 Sequence 18, Appli
C 27 139.2 2.1 7653 7 US-08-368-704A-1 Sequence 1, Appli
C 28 139.2 2.1 7653 7 US-08-368-704B-1 Sequence 1, Appli
C 29 139.2 2.1 7653 7 US-08-394-189-1 Sequence 1, Appli
C 30 139.2 2.1 7653 8 US-08-459-455-1 Sequence 1, Appli
C 31 139.2 2.1 7653 13 US-08-954-763-1 Sequence 1, Appli
C 32 139.2 2.1 7653 14 US-09-083-662-1 Sequence 1, Appli
C 33 139.2 2.1 7653 21 US-09-549-066-1 Sequence 18, Appli
C 34 139.2 2.1 7653 22 US-09-577-897-18 Sequence 1, Appli
C 35 139.2 2.1 7653 33 US-09-888-243-1 Sequence 1, Appli
C 36 122.8 1.9 6559 3 US-07-927-681-1 Sequence 1, Appli
C 37 122.8 1.9 6559 6 US-08-288-295-1 Sequence 1, Appli
C 38 122.8 1.9 6559 12 US-08-801-248-1 Sequence 1, Appli
C 39 122.8 1.9 6560 37 US-09-993-420A-1 Sequence 29178, A
C 40 121.4 1.8 42521 1 PCT-US00-14462A-23 Sequence 23, Appli
C 41 121 1.8 42521 1 PCT-US99-01313-23 Sequence 23, Appli
C 42 121 1.8 42521 1 PCT-US00-14462A-23 Sequence 23, Appli
C 43 121 1.8 42521 16 US-09-235-810-23 Sequence 23, Appli
C 44 121 1.8 42521 17 US-09-373-658-23 Sequence 23, Appli
C 45 121 1.8 42521 17 US-09-373-658B-23 Sequence 23, Appli
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ALIGNMENTS

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RESULT 1
US-09-993-420A-1
: Sequence 1, Application US/09993420A
: GENERAL INFORMATION:
: APPLICANT: Horvitz, H. Robert
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
: TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: 01997/201006
: CURRENT APPLICATION NUMBER: US-09/993,420A
: CURRENT FILING DATE: 5001-11-09
: PRIOR APPLICATION NUMBER: 09/234,186
: PRIOR FILING DATE: 1999-01-20
: PRIOR APPLICATION NUMBER: 07/898,933
: PRIOR FILING DATE: 1992-06-12
: PRIOR APPLICATION NUMBER: 07/927,681
: PRIOR FILING DATE: 1992-08-10
: PRIOR APPLICATION NUMBER: 08/288,295
: PRIOR FILING DATE: 1994-08-10
: PRIOR APPLICATION NUMBER: 08/801,248
: PRIOR FILING DATE: 1997-02-19
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 6560
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(6559)
: OTHER INFORMATION: n = A,T,C or G
US-09-993-420A-1
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Query Match 99.7%; Score 6541.8; DB 37; Length 6560;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGCATAGCTGTCACCAATGATTTTCGATTTCTCAGTGCATGCGTCAACAATTTA 60
Db 1 ATGCATAGCTGTCACCAATGATTTTCGATTTCTCAGTGCATGCGTCAACAATTTA 60
Qy 61 CAAATCTCGAAGAAAGAGATGCAAGAGTATGAGAGGTTCCGATCTAAATATTT 120
Db 1141 GAGAGAAATCGGATTCGACAGTTTGGCGTTGATTCACGCGTTTGTGATTCACCGT 1200
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Db 61 CAAATCTCGAAGAAAGAGATGCAAGAGTATGAGAGGTTCCGATCTAAATATTT 120
Qy 121 TAATTAATAAATCAATTTGATTTGAATTTGAATTTCACTACTGTTTGAATAAGCCAA 180
Db 121 TAATTAATAAATCAATTTGATTTGAATTTGAATTTCACTACTGTTTGAATAAGCCAA 180
Qy 181 TCCTTTAAGTAAGTCTGATTCGAGCCATTTCTTCCAGAAATTCCTTCAAGTGTGTT 240
Db 181 TCCTTTAAGTAAGTCTGATTCGAGCCATTTCTTCCAGAAATTCCTTCAAGTGTGTT 240
Qy 241 TTGTCATGATTTCCCGCCCAAGAAATGGAATTCGATTCCTGAGCAAGCGGAT 300
Db 241 TTGTCATGATTTCCCGCCCAAGAAATGGAATTCGATTCCTGAGCAAGCGGAT 300
Qy 301 TTTSATTAACAAAAAATCTATTCAGAACAAATAGACTTTTTCAAATATCTTATTTGG 360
Db 301 TTTSATTAACAAAAAATCTATTCAGAACAAATAGACTTTTTCAAATATCTTATTTGG 360
Qy 361 CTGTCCATTTGGAGACCCCAATCTTTAAGCTGTCCAGCCAGAAAGCTCCAGTGGCA 420
Db 361 CTGTCCATTTGGAGACCCCAATCTTTAAGCTGTCCAGCCAGAAAGCTCCAGTGGCA 420
Qy 421 AGGATTAAGAGGCTCAATTTTGAAGCCGAATTTACTAATATCTAGCCATGAGTGGAT 480
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Qy 481 GGATCAGAAATTCAGAGAAATTTAGATTTCACTTGAATTTGCAATGCAAAAAATATTT 540
Db 481 GGATCAGAAATTCAGAGAAATTTAGATTTCACTTGAATTTGCAATGCAAAAAATATTT 540
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Db 541 ATTCAAGAAATTCAGAGAAATTCAGAGAAATTCAGAGAAATTCAGAGAAATTCAGAGT 600
Qy 601 GAAAGTGCGCCCGGAGTGTGTCAGCATCTTTCAACAGAGACGCTGCTGGCGC 660
Db 601 GAAAGTGCGCCCGGAGTGTGTCAGCATCTTTCAACAGAGACGCTGCTGGCGC 660
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Db 721 CCGCCCTGTTCTTTTCAATTTGATTAAGAAATTCAGATTTTTCAGATGATTTAC 780
Qy 781 ATTCAAGTGCATGCTGTCGCGCTGCGGCGCAGATGCTGATTTCCGCTCTTGA 840
Db 781 ATTCAAGTGCATGCTGTCGCGCTGCGGCGCAGATGCTGATTTCCGCTCTTGA 840
Qy 841 ACATGATGCTGTCACCAAGTGGGATTTTGAATTTTCCGTGAATTTGTTGATTTT 900
Db 841 ACATGATGCTGTCACCAAGTGGGATTTTGAATTTTCCGTGAATTTGTTGATTTT 900
Qy 901 TGATGATGCTGTCAGAGAAATGATTAACAGACATCTTTCAATTAATTAATTA 960
Db 901 TGATGATGCTGTCAGAGAAATGATTAACAGACATCTTTCAATTAATTAATTA 960
Qy 961 TATTCAGATGTCAGAGCAAGAGCCCAATTCAGAGATTTGGATGGGATTCGTTGAG 1020
Db 961 TATTCAGATGTCAGAGCAAGAGCCCAATTCAGAGATTTGGATGGGATTCGTTGAG 1020
Qy 1021 CAGCGCTCCAGAAATGCGCCCAATGCTCCACATCTGACGCTACAGCACAATTTGACC 1080
Db 1021 CAGCGCTCCAGAAATGCGCCCAATGCTCCACATCTGACGCTACAGCACAATTTGACC 1080
Qy 1081 TGATGATGCTGTCAGATTCATAGATCAGAGGTTTGTATGAGCGGAAACCTTCTGTC 1140
Db 1081 TGATGATGCTGTCAGATTCATAGATCAGAGGTTTGTATGAGCGGAAACCTTCTGTC 1140
Qy 1141 GAGAGAAATCGGATTCGACAGTTTGGCGTTGATTCACGCGTTTGTGATTCACCGT 1200
Db 1141 GAGAGAAATCGGATTCGACAGTTTGGCGTTGATTCACGCGTTTGTGATTCACCGT 1200
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QY	1201	ACCTGGAACCTTACATGCGGGGTGACCGCTGTCTTCAAGTACATCATTCCTTTCCCATC	1260
Db	1201	ACCTGGAACCTTACATGCGGGGTGACCGCTGTCTTCAAGTACATCATTCCTTTCCCATC	1260
QY	1261	ATTTCCTCACTCTTAACGGAAATCGCTTCTTAGGANTGATTTGGCTAAGGAACTCAAT	1320
Db	1261	ATTTCCTCACTCTTAAACGGAAATCGCTTCTTAGGANTGATTTGGCTAAGGAACTCAAT	1320
QY	1321	AAATGTTGACAGGTAGAGAGTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1380
Db	1321	AAATGTTGACAGGTAGAGAGTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1380
QY	1381	TTCCAACTCAAAATCCGGGAATTCGTATCTGAGACTTTCGGCTATCTTCTGCTCTGCCA	1440
Db	1381	TTCCAACTCAAAATCCGGGAATTCGTATCTGAGACTTTCGGCTATCTTCTGCTCTGCCA	1440
QY	1441	TTGCTTTCAACTCTTGCCAGACACAGACACAAAGACTGCTTACGACAGATGCTCGGC	1500
Db	1441	TTGCTTTCAACTCTTGCCAGACACAGACACAAAGACTGCTTACGACAGATGCTCGGC	1500
QY	1501	TTCTTTTCTTCTTACTCGCCCCAGCCCTCGACAATTCGTCAATTTACTTTTACCCTTG	1560
Db	1501	TTCTTTTCTTCTTACTCGCCCCAGCCCTCGACAATTCGTCAATTTACTTTTACCCTTG	1560
QY	1561	ATTCTTGATTTTCTCTCTTTTCCGAGATTAACCTCCCTCTGCTTTTCTTCTCT	1620
Db	1561	ATTCTTGATTTTCTCTCTTTTCCGAGATTAACCTCCCTCTGCTTTTCTTCTCT	1620
QY	1621	GCTAGAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1680
Db	1621	GCTAGAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1680
QY	1681	GCGGCAACCTGCTGAGAGATCCGGGGTATCGGCCACGACATGGCGATGCGGAGATG	1740
Db	1681	GCGGCAACCTGCTGAGAGATCCGGGGTATCGGCCACGACATGGCGATGCGGAGATG	1740
QY	1741	AAGGACTTTCTGSGGATTAATAAGGCACAGACCCACCGATTTTGGAAATCAATAGTATCT	1800
Db	1741	AAGGACTTTCTGSGGATTAATAAGGCACAGACCCACCGATTTTGGAAATCAATAGTATCT	1800
QY	1801	CAGAGCTTCCCATACCCGAGTAGGCAGAGCTTGCAGCGGAAGATTCATCGGAGATCA	1860
Db	1801	CAGAGCTTCCCATACCCGAGTAGGCAGAGCTTGCAGCGGAAGATTCATCGGAGATCA	1860
QY	1861	ATTGATGGAAAAATCAATGATTTGGGAAGCCAGGCTGATGAGGAGATTTGTGTA	1920
Db	1861	ATTGATGGAAAAATCAATGATTTGGGAAGCCAGGCTGATGAGGAGATTTGTGTA	1920
QY	1921	ATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	1980
Db	1921	ATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	1980
QY	1981	CACCGAATCCGGGCAAAAACGGAATGGAATGTTTGAAGCACCGGGATTCGGCTGTGAGTG	2040
Db	1981	CACCGAATCCGGGCAAAAACGGAATGGAATGTTTGAAGCACCGGGATTCGGCTGTGAGTG	2040
QY	2041	CAACCGAGACGAAATGATGCGAGTATTTGGAGACGATTTTGGAAAGAACACCGCGAA	2100
Db	2041	CAACCGAGACGAAATGATGCGAGTATTTGGAGACGATTTTGGAAAGAACACCGCGAA	2100
QY	2101	AAATTTGAGACCTTCTGTGAGCAGCTGCTGCGAGTGCACAGATTCATTTCACTGTAT	2160
Db	2101	AAATTTGAGACCTTCTGTGAGCAGCTGCTGCGAGTGCACAGATTCATTTCACTGTAT	2160
QY	2161	CAGGATTTGTTGGGACGGTGGAAATGACACAGATCAATGTCCATGTCTTTAAGGA	2220
Db	2161	CAGGATTTGTTGGGACGGTGGAAATGACACAGATCAATGTCCATGTCTTTAAGGA	2220
QY	2221	CGTTTGGTAAGGAGAAAATACTGAAAAAAATTTGCAAAAAATTCGAAATTCGCCAGAA	2280
Db	2221	CGTTTGGTAAGGAGAAAATACTGAAAAAAATTTGCAAAAAATTCGAAATTCGCCAGAA	2280

QY	2281	AGGTGGCGAGAAAAACATTTGCCAAAATTTGTTGTTTCTCTTCAGAAATTCGCAAACT	2340
Db	2281	AGGTGGCGAGAAAAACATTTGCCAAAATTTGTTGTTTCTCTTCAGAAATTCGCAAACT	2340
QY	2341	TGGTCAAAATAGCCCAATTTGTGCTTTTGTGAAGTTTCCATTAAAAAAACACGAA	2400
Db	2341	TGGTCAAAATAGCCCAATTTGTGCTTTTGTGAAGTTTCCATTAAAAAAACACGAA	2400
QY	2401	TTTTGATCCCGATTGTATTTTTTTTGTGTGATTAATTCAGAGAAACTTTACGAATTCG	2460
Db	2401	TTTTGATCCCGATTGTATTTTTTTTGTGTGATTAATTCAGAGAAACTTTACGAATTCG	2460
QY	2461	ATTAAAAACGTTATTTCTATTCGAATTTTTTAAAGCATATTTTCCGTGATTTGATTT	2520
Db	2461	ATTAAAAACGTTATTTCTATTCGAATTTTTTAAAGCATATTTTCCGTGATTTGATTT	2520
QY	2521	CGGAAAAAGATCTGCTGATTTATCAAAAATCGTTTTAAATGTAAATTTGTGAAAAAT	2580
Db	2521	CGGAAAAAGATCTGCTGATTTATCAAAAATCGTTTTAAATGTAAATTTGTGAAAAAT	2580
QY	2581	ACATTAAATTCGATTTTGTGAACTTTTCTTGAAAAACAGTTTCTGCTGATTTTCG	2640
Db	2581	ACATTAAATTCGATTTTGTGAACTTTTCTTGAAAAACAGTTTCTGCTGATTTTCG	2640
QY	2641	TGAGGTAATTTTCCGCGACAGAAATGAGACGAATTAATTCGCAATTTCTATTTTCAGATA	2700
Db	2641	TGAGGTAATTTTCCGCGACAGAAATGAGACGAATTAATTCGCAATTTCTATTTTCAGATA	2700
QY	2701	TGAGGTAATTTTCCGCGACAGAAATGAGACGAATTAATTCGCAATTTCTATTTTCAGATA	2760
Db	2701	TGAGGTAATTTTCCGCGACAGAAATGAGACGAATTAATTCGCAATTTCTATTTTCAGATA	2760
QY	2761	GGTCTAATCTGTTCCGGCGGTTTCGTAGCTGCAAAAATATGAGAAATCCGTGGAACTCGAG	2820
Db	2761	GGTCTAATCTGTTCCGGCGGTTTCGTAGCTGCAAAAATATGAGAAATCCGTGGAACTCGAG	2820
QY	2821	GSACAAAGTCGCAAACTCTTCGTTTACACATGCTGTTCATCAAAAACGCGATCCGCAC	2880
Db	2821	GSACAAAGTCGCAAACTCTTCGTTTACACATGCTGTTCATCAAAAACGCGATCCGCAC	2880
QY	2881	AACTGGAAGGAAACAAATTCGAGCTGGGTAAAGAGATTTGATAGACATTTGAAGCTAA	2940
Db	2881	AACTGGAAGGAAACAAATTCGAGCTGGGTAAAGAGATTTGATAGACATTTGAAGCTAA	2940
QY	2941	TATCCCTTTCCTTACTACCTTACCTCCGGGGTGTGTTAAGCCGATTAATTACAGG	3000
Db	2941	TATCCCTTTCCTTACTACCTTACCTCCGGGGTGTGTTAAGCCGATTAATTACAGG	3000
QY	3001	GTTGCGTAGCCTCTTGGGGGGACAGCTGGGAACATTTCACTAATTAATCTGTTATGAT	3060
Db	3001	GTTGCGTAGCCTCTTGGGGGGACAGCTGGGAACATTTCACTAATTAATCTGTTATGAT	3060
QY	3061	AATGTTATTTGTACGGGAATCAAAAATTCGCAGAAATGCTATTTCACAAATATTGAGCG	3120
Db	3061	AATGTTATTTGTACGGGAATCAAAAATTCGCAGAAATGCTATTTCACAAATATTGAGCG	3120
QY	3121	GCAAAATATTCAGTAGAGAAACTACAGATATTTCTTAATTTTAAATTTTTCACATTT	3180
Db	3121	GCAAAATATTCAGTAGAGAAACTACAGATATTTCTTAATTTTAAATTTTTCACATTT	3180
QY	3181	AAAGAAATATACCACTATCAAAAAGAAATTAATTTCAAAAATTCGAGCCCGTAATTCGACT	3240
Db	3181	AAAGAAATATACCACTATCAAAAAGAAATTAATTTCAAAAATTCGAGCCCGTAATTCGACT	3240
QY	3241	ACAGTAGGCATTTAAGAAATTTACTGTAGTTTTCGCTAGACATATTTCCGCTCAAAATAT	3300
Db	3241	ACAGTAGGCATTTAAGAAATTTACTGTAGTTTTCGCTAGACATATTTCCGCTCAAAATAT	3300
QY	3301	GTTGTGAAATATACGATTCACAGGATTTTGTGTTTCCCGGAATATGCTTTAAAGCATTAAT	3360
Db	3301	GTTGTGAAATATACGATTCACAGGATTTTGTGTTTCCCGGAATATGCTTTAAAGCATTAAT	3360
QY	3361	TGTGAAATATTAATAATCAAGAAAAAATTTGACGAGCACTTCATGACCTCGAAAAACA	3420

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Db 3361 TGTGAAAATATATAAATAAATAAATTCAGAGACACTTCATGACACTCGGAAAAA 3420
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Qy 3421 ATGAAGAGACTACGAAACGACGAGAACTGAAAAAGTGGAGCCGGAAGCAGACAGA 3480
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Db 3421 ATGAAGAGAGACTACGAAACGAGAACTGAAAAAGTGGAGCCGGAAGCAGACAGA 3480
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Qy 3481 CGGTGCTGATGATGGCGCTGGAGTACAGCTGAGACCATTTGGAATCGTTGGAGTGTG 3540
|||||
Db 3481 CGGTGCTGATGATGGCGCTGGAGTACAGCTGAGACCATTTGGAATCGTTGGAGTGTG 3540
|||||
Qy 3541 GTGTGGGGGAGATGATGCTGAGCTGAAAGTAACTGATTAATTTGTAATTAATTAAT 3600
|||||
Db 3541 GTGTGGGGGAGATGATGCTGAGCTGAAAGTAACTGATTAATTTGTAATTAATTAAT 3600
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Qy 3601 TTATGTAACAACCTCTTACATTTGTAATCTCATTTTGTCTCAGTATCTCATCTTTGA 3660
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Db 3601 TTATGTAACAACCTCTTACATTTGTAATCTCATTTTGTCTCAGTATCTCATCTTTGA 3660
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Qy 3661 ACTGGAAGAGTGGGAAGCTAGGCGCAAAATTCAGGCTGCTGCTGCTGATTTACGATT 3720
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Db 3661 ACTGGAAGAGTGGGAAGCTAGGCGCAAAATTCAGGCTGCTGCTGCTGATTTACGATT 3720
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Qy 3721 TACTGCAATTTTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3780
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Qy 3781 ACTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3840
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Db 3781 ACTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3840
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Qy 3841 GCGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3900
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Db 3901 TTCACTTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3960
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Qy 3961 GTAGCGCACTTGTATTTATTTTTCGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4020
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Db 3961 GTAGCGCACTTGTATTTATTTTTCGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4020
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Db 4561 CTTAAATTTGAAGTTTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4620
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Db 4621 GAGATTTTCAATTAATTTGATTTGAAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCA 4680
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Db 4741 TTAATTTCAAAAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4800
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Qy 4801 GGAATTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4860
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Db 4801 GGAATTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4860
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Db 4861 AAATTTAATTTTACCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4920
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 QY 5821 GAAAGCCGTGAATTTTAACTTGAACGTGATAGAGAAAGTTCGTGATTAATGAGCAAT 5880
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 QY 5881 TTTGCCAGTATATCTTTGTGATATCAGATTAACGAGTCAAGCAAGCAAGCAATATTA 5940
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 Db 5881 TTTGCCAGTATATCTTTGTGATATCAGATTAACGAGTCAAGCAAGCAAGCAATATTA 5940
 QY 5941 GAAACACAAATTAATGAGAAATGGGCAACATATTTGACCGCAAAATATCTGATGCGAAA 6000
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 Db 5941 GAAACACAAATTAATGAGAAATGGGCAACATATTTGACCGCAAAATATCTGATGCGAAA 6000
 QY 6001 CTACAGTATTTCTTCAAAAGCACTACTGAGCGCTGTGTCATTTACGAGCTCGATTTTGG 6060
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 Db 6001 CTACAGTATTTCTTCAAAAGCACTACTGAGCGCTGTGTCATTTACGAGCTCGATTTTGG 6060
 QY 6061 AAATGAATCAGACTAGAGAAAGAGAGAAATATTTGACATCAATGAACATCAATTTCA 6120
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 Db 6061 AAATGAATCAGACTAGAGAAAGAGAGAAATATTTGACATCAATGAACATCAATTTCA 6120
 QY 6121 AAAAGTGAACCCCTTGACATGATAGTCTTCAAAAGAAATTTAGTCTGCTGACGAG 6180
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 Db 6121 AAAAGTGAACCCCTTGACATGATAGTCTTCAAAAGAAATTTAGTCTGCTGACGAG 6180
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 QY 6241 TGTCTGAAAAATTTTCATTTCAACATCAATTAAGCAAAATCTAAAAATTTGGGTTCTGCA 6300
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 QY 6301 GCGACCACTATGACTGATCGTGGCAAGCACTCAGAAAACTAGCTGTTCTTTAA 6360
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 Db 6301 GCGACCACTATGACTGATCGTGGCAAGCACTCAGAAAACTAGCTGTTCTTTAA 6360
 QY 6361 CAATATCATTTTAAATGATTTGATTAATAATTTGTTGCTGAGCTGATAGCTGCTT 6420
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 Db 6361 CAATATCATTTTAAATGATTTGATTAATAATTTGTTGCTGAGCTGATAGCTGCTT 6420
 QY 6421 TTTTCACTGCAAACTCTTAATTTAATCGCGGCTCTTCAAAAAGTCGTTTCTTGAAAA 6480
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 Db 6421 TTTTCACTGCAAACTCTTAATTTAATCGCGGCTCTTCAAAAAGTCGTTTCTTGAAAA 6480
 QY 6481 TATTAAGCTTATATATTTATATATTAATAATTTTATATATATATCAAAAGCAGCTA 6540
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 Db 6481 TATTAAGCTTATATATTTATATATTAATAATTTTATATATATATCAAAAGCAGCTA 6540
 QY 6541 GTTTGTATATAAATTTATCA 6560
 |||||
 Db 6541 GTTTGTATATAAATTTATCA 6560
 RESULT 2
 US-07-927-681-1
 ; Sequence 1, Application US/07927681

GENERAL INFORMATION:
 APPLICANT: Horvitz, H. Robert
 TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL
 DEATH AND USES THEREFOR
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P. C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02173-4799
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/927,681
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: MIT-5934A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 861-6240
 TELEFAX: (617) 861-9540
 TELEX: 951794
 INFORMATION FOR SEQ. ID NO. 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6559 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-07-927-681-1
 Query Match 99.5%; Score 6529, 8; DB 3; Length 6559;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 6559; Conservative 0; Mismatches 0; Indels 1; Gaps 1:
 QY 1 ATCGATAGTCGTCACCAATTTTCCGATTTCTCAGTACTGATGCTGACAAATTTA 60
 |||||
 Db 1 ATCGATAGTCGTCACCAATTTTCCGATTTCTCAGTACTGATGCTGACAAATTTA 60
 QY 61 CAAATCTCGAAGAAAGAGATGCAAGGATATGAGAGAGTTCCGAATCTAAATATT 120
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 Db 61 CAAATCTCGAAGAAAGAGATGCAAGGATATGAGAGAGTTCCGAATCTAAATATT 120
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|||||
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OY
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Db
2580 ACATTAATAATTCGATTTTGAATTTTCTTCGAAAAACAGGTTTTCGCTGATTTGC 2639
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DB 2640 TGAACAAAAAACCACAAATTCATTTTCGAACATTTAAACGAAAAATCGTTTTT 2699
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DB 2700 TAAGCTTAATTTTCCGCGCAAAATGAACGAATTAATTTGCAAAATTTCTAATTTTCAGATA 2759
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DB 2760 GGTCTAATCTGTTGCGCGGTTTCGAGTCGCAAAAAATGATGGAATCCGTGCAATCGCAG 2819
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DB 2820 GGAACAGTGGAAACCTCTTCGTTTACACATCCCTGTTCAATCAAAACGGGAGATCCGCAAC 2879
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DB 2940 TATCCCTTTCCCTAGTACCTTGAATCCCGGGGTGTGTAAGCCGATTAATTCAGG 2999
OY 3001 GTTGGGATGACCTTTGGGGGAGACGTGGAACATATTCAGATATTTACTGTTTATGAT 3060
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DB 3120 GCAAAATATCCAGTAGAGAAAATCTACGTAATTTCTTAAATTTTAAATTTTACAT 3179
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DB 3180 AAAAATAATACGCACTATCAAAAATTAATTTCAAAAATGAGCCGCAATTCAGCT 3239
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DB 3240 ACAGTAGCATTTAAAGATTTCTGATTTTCCCTACAGATATTTCCGCTCAATAT 3299
OY 3301 GTTGGAAATACGATTCACGAGATTTTGTCTCCCGGAATATGCTTAAAGCATTAT 3360
DB 3300 GTTGGAAATACGATTCACGAGATTTTGTCTCCCGGAATATGCTTAAAGCATTAT 3359
OY 3361 TGTGAATTAATAAATCAAGAAAAAATTCGAGACGATTCATGACACTCGAAAAA 3420
DB 3360 TGTGAATTAATAAATCAAGAAAAAATTCGAGACGATTCATGACACTCGAAAAA 3419
OY 3421 ATGAAGAAGACACTACAGACAGCAGACGCTGAAAAAGTGGAGCCGAGACACAGACA 3480
DB 3420 ATGAAGAAGACACTACAGACAGCAGACGCTGAAAAAGTGGAGCCGAGACACAGACA 3479
OY 3481 CGGTGCTGATGATGGGGGCTGGAGTACACGCTGGAGCCATTTGGAATGTTGGAGTCTC 3540
DB 3480 CGGTGCTGATGATGGGGGCTGGAGTACACGCTGGAGCCATTTGGAATGTTGGAGTCTC 3539
OY 3541 GTGTGTGGCGGATGATGTTGAGTTGAAGTAACTATTTCAATTTGTGTAATTAATTAAT 3600
DB 3540 GTGTGTGGCGGATGATGTTGAGTTGAAGTAACTATTTCAATTTGTGTAATTAATTAAT 3599
OY 3601 TTATGTACACCTCTTACATTTGAATTCATTTTTCCTACCTGATTCCTCATCCTTTGA 3660
DB 3600 TTATGTACACCTCTTACATTTGAATTCATTTTTCCTACCTGATTCCTCATCCTTTGA 3659
OY 3661 ACTGAAGAAGTGGAAACCTAGCCACAAATTAAGGCTCTCTGTGTGATTTAGATTT 3720
DB 3660 ACTGAAGAAGTGGAAACCTAGCCACAAATTAAGGCTCTCTGTGTGATTTAGATTT 3719

OY 3721 TACTGCATTTTTCGATTCGCTTTTGTGGCAAAACCTTACTTCGCGTAATATCA 3780
DB 3720 TACTGCATTTTTCGATTCGCTTTTGTGGCAAAACCTTACTTCGCGTAATATCA 3779
OY 3781 ACTTTCCGTTGTTGTAATTTTGTGCAAAAACCTGAAACCTTCTTCGCGGTG 3840
DB 3780 ACTTTCCGTTGTTGTAATTTTGTGCAAAAACCTGAAACCTTCTTCGCGGTG 3839
OY 3841 GCTTACCTCCGCTTCTCTTCCACATTTCCAAAGTAACTCCCTGATCTCAATTAATTCATC 3900
DB 3840 GCTTACCTCCGCTTCTCTTCCACATTTCCAAAGTAACTCCCTGATCTCAATTAATTCATC 3899
OY 3901 TTCATTTTACCTCTCTTTCGTTGCTGCTTCCACTCCCAATTTCTGTAACG 3960
DB 3900 TTCATTTTACCTCTCTTTCGTTGCTGCTTCCACTCCCAATTTCTGTAACG 3959
OY 3961 GTACGCGATTTGTAATTTTTCGAAATTTGTTTCTCTCTCAACACAAAAAATAC 4020
DB 3960 GTACGCGATTTGTAATTTTTCGAAATTTGTTTCTCTCTCAACACAAAAAATAC 4019
OY 4021 GGTCTTTTATCAACCTTTTTCGAAACGAACTGCAATTTGATAGCGCTGCGC 4080
DB 4020 GGTCTTTTATCAACCTTTTTCGAAACGAACTGCAATTTGATAGCGCTGCGC 4079
OY 4081 AAGAGATCCGTTTTCATTTTCCCATCAGCTCATCCAAAAAGTTTATGAGAAAAATA 4140
DB 4080 AAGAGATCCGTTTTCATTTTCCCATCAGCTCATCCAAAAAGTTTATGAGAAAAATA 4139
OY 4141 TCATTTTATATATATGATTCATCTTCTGCGCTCTGCTGAGACGAGCTCAAT 4200
DB 4140 TCATTTTATATATATGATTCATCTTCTGCGCTCTGCTGAGACGAGCTCAAT 4199
OY 4201 TCGATGCTTGAATTTTTCGAAAAAATGTTTGTAGTATGTAAGATCCCCC 4260
DB 4200 TCGATGCTTGAATTTTTCGAAAAAATGTTTGTAGTATGTAAGATCCCCC 4259
OY 4261 GCCTTATGCTGTTTACCATCATAGATAGGCTCCGCAATTTGATTTCCCTTGAATTTTTCG 4320
DB 4260 GCCTTATGCTGTTTACCATCATAGATAGGCTCCGCAATTTGATTTCCCTTGAATTTTTCG 4319
OY 4321 GTATATTAATAAAGTAAAGTTAGTGCAGATTCAAAAAACAATTCGCTTACTAT 4380
DB 4320 GTATATTAATAAAGTAAAGTTAGTGCAGATTCAAAAAACAATTCGCTTACTAT 4379
OY 4381 TCACTCTGTTGTTCTTTTGGCTTTTGGCTTTGTTGAGGCAAGACGACTATCAGT 4440
DB 4380 TCACTCTGTTGTTCTTTTGGCTTTTGGCTTTGTTGAGGCAAGACGACTATCAGT 4439
OY 4441 TCAAGGTTACACTATTTTGAATTAAGAGAAATTCAGGMRAGGTTACCTTGGAGAA 4500
DB 4440 TCAAGGTTACACTATTTTGAATTAAGAGAAATTCAGGMRAGGTTACCTTGGAGAA 4499
OY 4501 AGATACCTGAGATTTTCACTCTGTTTGAAGTAAAGGCTTAAAGAGACTTAAAGAG 4560
DB 4500 AGATACCTGAGATTTTCACTCTGTTTGAAGTAAAGGCTTAAAGAGACTTAAAGAG 4559
OY 4561 CCTAAAAATTAAGTTCACCTGTTTCAAAAGAAAGCCGATTTGACAGCTTTACAC 4620
DB 4560 CCTAAAAATTAAGTTCACCTGTTTCAAAAGAAAGCCGATTTGACAGCTTTACAC 4619
OY 4621 GAGATTTCTCAATTAATTTGTAATTTGAATTTTCAATTTTCCCAAGAGTCTTTACAC 4680
DB 4620 GAGATTTCTCAATTAATTTGTAATTTGAATTTTCAATTTTCCCAAGAGTCTTTACAC 4679
OY 4681 GAAATTTTGCATTTTTCGACTTAAATATACGATACCTGCTGACACGAAACATTTTTCG 4740
DB 4680 GAAATTTTGCATTTTTCGACTTAAATATACGATACCTGCTGACACGAAACATTTTTCG 4739
OY 4741 TTAATTTCAAAAGATGTTGGCTTTTAAAGAGTCTTAAAGTCTGTTGAGAACTCTCTGTTTCG 4800
DB 4740 TTAATTTCAAAAGATGTTGGCTTTTAAAGAGTCTTAAAGTCTGTTGAGAACTCTCTGTTTCG 4799
OY 4801 GGACTTTTCAATGATTTTTCGATGCGTTTATTAAGAAAAATGATTTATTTATTCAA 4860

APPLICATION NUMBER: US 07/927,681
FILING DATE: 10-AUG-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 01997/201003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6559 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-285-1

Query Match 99.5%; Score 6529.8; DB 6; Length 6559;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6559; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATCGATGTCGTCACCAATGATGATTTCCGATTTCTCAGTACGATGCTCACAATTTA 60
DB 1 ATCGATGTCGTCACCAATGATGATTTCCGATTTCTCAGTACGATGCTCACAATTTA 60
QY 61 CAAAATCTCGAAGAAAGAAAGATGCAAGAGATGCAAGAGATGCAAGAGATGCAAG 120
DB 61 CAAAATCTCGAAGAAAGAAAGATGCAAGAGATGCAAGAGATGCAAGAGATGCAAG 120
QY 121 TAATTTAAAAAATCAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTT 180
DB 121 TAATTTAAAAAATCAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTT 180
QY 181 TCCCTTAAGTAACTCTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGAT 240
DB 181 TCCCTTAAGTAACTCTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGAT 240
QY 241 TTGCTAGTATTTCTGTCGCAAGAAATAGAAATGAAATGAAATGAAATGAAATG 300
DB 241 TTGCTAGTATTTCTGTCGCAAGAAATAGAAATGAAATGAAATGAAATGAAATG 300
QY 301 TTTSATTAACAAAACATCTCCAGCAACCAATGAGACTTTTCAATTAATCTTAAT 360
DB 301 TTTSATTAACAAAACATCTCCAGCAACCAATGAGACTTTTCAATTAATCTTAAT 360
QY 361 CTGTCATTTGGAAGCAACCAATCTTTAAGCTGTCCAGCGCAGAAAGTCTCCACTG 420
DB 361 CTGTCATTTGGAAGCAACCAATCTTTAAGCTGTCCAGCGCAGAAAGTCTCCACTG 420
QY 421 AGATTAAGAGCTATTTTGAAGCCGAATTTTACTAAATCTTACCAATGAGTGTAT 480
DB 421 AGATTAAGAGCTATTTTGAAGCCGAATTTTACTAAATCTTACCAATGAGTGTAT 480
QY 481 GGATGAGAAATTCGAGAAATTTAGATTTGATTTGATTTGATTTGATTTGATTTGAT 540
DB 481 GGATGAGAAATTCGAGAAATTTAGATTTGATTTGATTTGATTTGATTTGATTTGAT 540
QY 541 ATTCAAGAAATTCAGAGAAATTCAGAGAAATTCAGAGAAATTCAGAGAAATTCAG 600
DB 541 ATTCAAGAAATTCAGAGAAATTCAGAGAAATTCAGAGAAATTCAGAGAAATTCAG 600
QY 601 GAAAGTGGCGCGGCTGTTGCTGAGAGCATCTTCAAGAGAGAGAGAGAGAGAGAG 660
DB 601 GAAAGTGGCGCGGCTGTTGCTGAGAGCATCTTCAAGAGAGAGAGAGAGAGAGAG 660
QY 661 ACTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 661 ACTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 CGGCCCTGTTCTTTTCAATTTGATTAAGAAATTCAGCATTTGTTTCAGATGATTA 780
DB 721 CGGCCCTGTTCTTTTCAATTTGATTAAGAAATTCAGCATTTGTTTCAGATGATTA 780

DB 720 CGGCCCTGTTCTTTTCAATTTGATTAAGAAATTCAGCATTTGTTTCAGATGATTA 779
QY 781 ATTCCAACTGCGATTTCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTG 840
DB 781 ATTCCAACTGCGATTTCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTG 839
QY 841 ACATGATGCTGACCAAGAGTGGGATTTTGAATTTTCCGTAATTTGTAATTTGTAAT 900
DB 841 ACATGATGCTGACCAAGAGTGGGATTTTGAATTTTCCGTAATTTGTAATTTGTAAT 899
QY 901 TGTGTACCATGAGAGAGAAATGATTAACAGACATTTCTTCAATTAATTAATTAAT 960
DB 901 TGTGTACCATGAGAGAGAAATGATTAACAGACATTTCTTCAATTAATTAATTAAT 959
QY 961 TATTTACAGTCCGAGAGCAACAGCCATTCAGAGATGCGATGCGATGCGATGCG 1020
DB 961 TATTTACAGTCCGAGAGCAACAGCCATTCAGAGATGCGATGCGATGCGATGCG 1019
QY 1021 CAGCGCTCCAGAAATCGCCCAATCGCTCCAGATCTCACCGTCTACAGCCCAAT 1080
DB 1021 CAGCGCTCCAGAAATCGCCCAATCGCTCCAGATCTCACCGTCTACAGCCCAAT 1079
QY 1081 TCGATGCTCTCCGATTTCCATTAAGATCAAGCGTTGTGAATGCGCGAATCTGCT 1140
DB 1081 TCGATGCTCTCCGATTTCCATTAAGATCAAGCGTTGTGAATGCGCGAATCTGCT 1139
QY 1141 GGAGAAATCGAGATGCGAGTTTGGCGTTCGATTTCAAGTATTCATTTATCCGT 1200
DB 1141 GGAGAAATCGAGATGCGAGTTTGGCGTTCGATTTCAAGTATTCATTTATCCGT 1199
QY 1201 AGCTGAACTTACATTCGCGGCTGACCGCTCTTCAAGTATTCATTTATCCGT 1260
DB 1201 AGCTGAACTTACATTCGCGGCTGACCGCTCTTCAAGTATTCATTTATCCGT 1259
QY 1261 ATTTTCATTTCTTAAGCAATTTGCTTTAGATTTGATTTGATTTGATTTGATTT 1320
DB 1261 ATTTTCATTTCTTAAGCAATTTGCTTTAGATTTGATTTGATTTGATTTGATTT 1319
QY 1321 AATGTTGAGAGATGAGATTTGAAATTAATTAATTTAATTTAATTTAATTTAAT 1380
DB 1321 AATGTTGAGAGATGAGATTTGAAATTAATTAATTTAATTTAATTTAATTTAAT 1379
QY 1381 TTTCAGATCTAACAATGCGGATTTCTGATTTGATTTGATTTGATTTGATTTGAT 1440
DB 1381 TTTCAGATCTAACAATGCGGATTTCTGATTTGATTTGATTTGATTTGATTTGAT 1439
QY 1441 TTGCTTTCAACTTTTCCAGAACAGAGCAACAGAGATTTGATTTGATTTGATTT 1500
DB 1441 TTGCTTTCAACTTTTCCAGAACAGAGCAACAGAGATTTGATTTGATTTGATTT 1499
QY 1501 TTCTTTTCTTACTCCGCGCCAGCCCTGACAAATTTCTGATTTTACTTTTACT 1560
DB 1501 TTCTTTTCTTACTCCGCGCCAGCCCTGACAAATTTCTGATTTTACTTTTACT 1559
QY 1561 ATTTCTGATTTTCTCTTTTCTGATTTTACTCTCTCTCTCTCTCTCTCTCTCT 1620
DB 1561 ATTTCTGATTTTCTCTTTTCTGATTTTACTCTCTCTCTCTCTCTCTCTCTCT 1619
QY 1621 GTCTAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1680
DB 1621 GTCTAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1679
QY 1681 GCGGAACTGCTGAGATTCGCGGATTCGCGAGAGATGCGAGATGCGAGATG 1740
DB 1681 GCGGAACTGCTGAGATTCGCGGATTCGCGAGAGATGCGAGATGCGAGATG 1739
QY 1741 AAGAGTTTCTGGGATTAAGAGCAACAGCCATTTTGAATTTGATTTGATTTGAT 1800
DB 1741 AAGAGTTTCTGGGATTAAGAGCAACAGCCATTTTGAATTTGATTTGATTTGAT 1799
QY 1801 CAGGACTTGCATCAGAGATGAGAGCTTCAGCCGGAAGATGCTATCGAGAGTCA 1860
DB 1801 CAGGACTTGCATCAGAGATGAGAGCTTCAGCCGGAAGATGCTATCGAGAGTCA 1860

Db 1800 CAGGACTGCCATCACCGAGTAGGACGCTTCGACGCGAAGATGTCATCGAGAGTCA 1859
QY 1861 ATTGATGAAAAATCATGATTTGGAGAGCCAAAGCTTGTGATTCAGAGGATTTGTGTA 1920
Db 1860 ATTGATGAAAAATCATGATTTGGAGAGCCAAAGCTTGTGATTCAGAGGATTTGTGTA 1919
QY 1921 ATTTTATTTTATTTTATTTTGTAAATTAATTTTCCTGCTGCTTCGAGGTCAGTATTTTCAG 1980
Db 1920 ATTTTATTTTATTTTATTTTGTAAATTAATTTTCCTGCTGCTTCGAGGTCAGTATTTTCAG 1979
QY 1981 CACGAAATCCGGCAAAACGGAATGGAATGTTGGAGACCGGGATTCGCCCTGTGGAGTC 2040
Db 1980 CACGAAATCCGGCAAAACGGAATGGAATGTTGGAGACCGGGATTCGCCCTGTGGAGTC 2039
QY 2041 CAACCGGAGCAGAAATGATGCGAGTATGGGAAAGATATTCGAGAAAGACAGCGGAA 2100
Db 2040 CAACCGGAGCAGAAATGATGCGAGTATGGGAAAGATATTCGAGAAAGACAGCGGAA 2099
QY 2101 AATTTTGAGACCTTCTGTGACAGCTGCTGCGAGTGCACAGATTCATTTTCAGTGTAT 2160
Db 2100 AATTTTGAGACCTTCTGTGACAGCTGCTGCGAGTGCACAGATTCATTTTCAGTGTAT 2159
QY 2161 CAGGATGCTGTTGGAGCGTTGGAAATGACAGACATCAATGCCAATGCTTATGCA 2220
Db 2160 CAGGATGCTGTTGGAGCGTTGGAAATGACAGACATCAATGCCAATGCTTATGCA 2219
QY 2221 CGTTTGTAGGAGGAAAAATACTGAAAAAAAGTTTGCAAAAATTCGAAAAATTCGCCGAA 2280
Db 2220 CGTTTGTAGGAGGAAAAATACTGAAAAAAAGTTTGCAAAAATTCGAAAAATTCGCCGAA 2279
QY 2281 AGGTGGCGAAAAAACATTTTGCAAAAATTTGTTTCTTCGGAATTCAGCAAACT 2340
Db 2280 AGGTGGCGAAAAAACATTTTGCAAAAATTTGTTTCTTCGGAATTCAGCAAACT 2339
QY 2341 TGGTCAAAAAATAGCCCATTTATGTCCTTTTGAAGTTTCCATTAATAAAACCAAGAA 2400
Db 2340 TGGTCAAAAAATAGCCCATTTATGTCCTTTTGAAGTTTCCATTAATAAAACCAAGAA 2399
QY 2401 TTTTGATCCGGATGTAATTTTGTGATTAATTAACAGAAAACTTTAGCAATTCG 2460
Db 2400 TTTTGATCCGGATGTAATTTTGTGATTAATTAACAGAAAACTTTAGCAATTCG 2459
QY 2461 ATTAAAAACGTTATTTCTATTCGAAATATTTTAAAGCATATTTTCTTATTTGATTT 2520
Db 2460 ATTAAAAACGTTATTTCTATTCGAAATATTTTAAAGCATATTTTCTTATTTGATTT 2519
QY 2521 GCGAAAAAGATGCTGCTGATTTATCAAAAAATCGTTTAAATGAAAAATTTGGAAAAAT 2580
Db 2520 GCGAAAAAGATGCTGCTGATTTATCAAAAAATCGTTTAAATGAAAAATTTGGAAAAAT 2579
QY 2581 ACATTAATAATTCATTTTGAATTTTCTTCTGAAAAACAGGTTTCTGCTGATTTGC 2640
Db 2580 ACATTAATAATTCATTTTGAATTTTCTTCTGAAAAACAGGTTTCTGCTGATTTGC 2639
QY 2641 TGAACGAAAAACCCAAAAATTCATTTTGAACATTAATAAACCAAAAAATTCGTTT 2700
Db 2640 TGAACGAAAAACCCAAAAATTCATTTTGAACATTAATAAACCAAAAAATTCGTTT 2699
QY 2701 TAAAGCTTAATTTTCCGACAAATGAACGATTAATTAATTCATTTTTCAGATA 2760
Db 2700 TAAAGCTTAATTTTCCGACAAATGAACGATTAATTAATTCATTTTTCAGATA 2759
QY 2761 GGTCTATCTCTGCTGGCGGTTTCGATGTCGAAAAATGAGATTCGTGAACTGCAG 2820
Db 2760 GGTCTATCTCTGCTGGCGGTTTCGATGTCGAAAAATGAGATTCGTGAACTGCAG 2819
QY 2821 GGAAGAAGTGAACCTCTGCTTACACATGCTGTATCAAAACGGGATTCGGCAAC 2880
Db 2820 GGAAGAAGTGAACCTCTGCTTACACATGCTGTATCAAAACGGGATTCGGCAAC 2879
QY 2881 AACTGGAAGAACACATGAGAGCTGGTAAAGAGTATTTGATAGCATTTAGAGTCA 2940
Db 2880 AACTGGAAGAACACATGAGAGCTGGTAAAGAGTATTTGATAGCATTTAGAGTCA 2939

QY 2941 TATCCCTTCCCTAGTACCTTGAATTCCTCCGGGCTGTTGGTAACCCGATATTAACAG 3000
Db 2940 TATCCCTTCCCTAGTACCTTGAATTCCTCCGGGCTGTTGGTAACCCGATATTAACAG 2999
QY 3001 GTTCGGTAGCCCTTGGGGGACAGCTGGAACATTTTCAAGATTAATTTACTGTTATGAT 3060
Db 3000 GTTCGGTAGCCCTTGGGGGACAGCTGGAACATTTTCAAGATTAATTTACTGTTATGAT 3059
QY 3061 AATGTTATTTGTTACGGGAATACAAAATTCGACAGATGATTTTCAACATATTTGAGCG 3120
Db 3060 AATGTTATTTGTTACGGGAATACAAAATTCGACAGATGATTTTCAACATATTTGAGCG 3119
QY 3121 GCAAAATATCCAGTACGAAATACAGTAATTTCTTAATTTTAAATTTTAAATTTTAAATTT 3180
Db 3120 GCAAAATATCCAGTACGAAATACAGTAATTTCTTAATTTTAAATTTTAAATTTTAAATTT 3179
QY 3181 AAGAAAAATACCACTAATTCAAAAGAAATTAATTTCAAAAATTCGAGCCGTAAATCGACT 3240
Db 3180 AAGAAAAATACCACTAATTCAAAAGAAATTAATTTCAAAAATTCGAGCCGTAAATCGACT 3239
QY 3241 ACAGTAGCATTTAAAGAAATTAATTTACTGATTTTTCGACAGATTAATTTCCGCTCAATAT 3300
Db 3240 ACAGTAGCATTTAAAGAAATTAATTTACTGATTTTTCGACAGATTAATTTCCGCTCAATAT 3299
QY 3301 GTTGGAATTAAGCATTCAGGATTTTGTGTTTCCCGGAAATATGCTTAAAGCATTTAT 3360
Db 3300 GTTGGAATTAAGCATTCAGGATTTTGTGTTTCCCGGAAATATGCTTAAAGCATTTAT 3359
QY 3361 TGTAAAAATAAAAATCAAGAAAAAATTCAGAGAGCACTTCATGACCTGGAAGAACAA 3420
Db 3360 TGTAAAAATAAAAATCAAGAAAAAATTCAGAGAGCACTTCATGACCTGGAAGAACAA 3419
QY 3421 ATGAAAGAGCACTACGAGAGCAGACAGAGCTGAAAAAGTGGGAGCGCGGAGCAGAACGA 3480
Db 3420 ATGAAAGAGCACTACGAGAGCAGACAGAGCTGAAAAAGTGGGAGCGCGGAGCAGAACGA 3479
QY 3481 CGTGGTCATGATTTGGGCTGAGTAAACAGCTGAGCATTTGAAATGTTGGAGTGTGTC 3540
Db 3480 CGTGGTCATGATTTGGGCTGAGTAAACAGCTGAGCATTTGAAATGTTGGAGTGTGTC 3539
QY 3541 GTGTGGGGGAGTATGTTGAGTGAAGTAACTTATTCATTTGTTGTAATTAATTAAT 3600
Db 3540 GTGTGGGGGAGTATGTTGAGTGAAGTAACTTATTCATTTGTTGTAATTAATTAAT 3599
QY 3601 TTATGTACACCTCTTACATTTGATTTGATTTTGTCTGACATGATTTCTATCTTGA 3660
Db 3600 TTATGTACACCTCTTACATTTGATTTGATTTTGTCTGACATGATTTCTATCTTGA 3659
QY 3661 ACTGGAAGAGTGGGAAAGCTAGGCAACAATTAACGCTCTGTGTCGATTTAGCATTT 3720
Db 3660 ACTGGAAGAGTGGGAAAGCTAGGCAACAATTAACGCTCTGTGTCGATTTAGCATTT 3719
QY 3721 TACTGCAATTTTTCGATGCTTTTGTGTCGCAAAACCTACTTCCGGTAAATCA 3780
Db 3720 TACTGCAATTTTTCGATGCTTTTGTGTCGCAAAACCTACTTCCGGTAAATCA 3779
QY 3781 ACTTTCGCTGCTGCTACATTTGCTGCAAAAACCTGAAACCTTAACCTTTTCTGCGGTG 3840
Db 3780 ACTTTCGCTGCTGCTACATTTGCTGCAAAAACCTGAAACCTTAACCTTTTCTGCGGTG 3839
QY 3841 GCTAGACCTCCGCTTCTCTCCACATTTCCAAAGTACCCCTGATTCATTAATTCATC 3900
Db 3840 GCTAGACCTCCGCTTCTCTCCACATTTCCAAAGTACCCCTGATTCATTAATTCATC 3899
QY 3901 TTCACTTTAATCTGCTCTTTTGTGTGGCTCTTCCAACTCCGCCCAATTCGTAGCG 3960
Db 3900 TTCACTTTAATCTGCTCTTTTGTGTGGCTCTTCCAACTCCGCCCAATTCGTAGCG 3959
QY 3961 GTAGCGCACTTGTATTAATTTTTCATTAATTTGTTTCTGTACACACACAAAAAAC 4020
Db 3960 GTAGCGCACTTGTATTAATTTTTCATTAATTTGTTTCTGTACACACACAAAAAAC 4019

QY 4021 GGTCTTTTATTCACCCCTTTTTCGAGCAAACTGCAATTTTGATTAATAGGCGTGGC 4080
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Db 4020 GGTCTTTTATTCACCCCTTTTTCGAGCAAACTGCAATTTTGATTAATAGGCGTGGC 4079
QY 4081 AAGGAATCCGGTTTTCATTTTGGCCATCAGTCATCCAAAAGTTTACTAGAAAATA 4140
|||||
Db 4080 AAGGAATCCGGTTTTCATTTTGGCCATCAGTCATCCAAAAGTTTACTAGAAAATA 4139
QY 4141 TCAATTTTATTAATGATTCATCTTCGCGCTCTCTGCTCGAGACGAGCTCAAT 4200
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Db 4140 TCAATTTTATTAATGATTCATCTTCGCGCTCTCTGCTCGAGACGAGCTCAAT 4199
QY 4201 TCGATGCCCTTGAATTTTTCGAAAACAAAATTTTGTAGTAAACGATCCGCC 4260
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Db 4200 TCGATGCCCTTGAATTTTTCGAAAACAAAATTTTGTAGTAAACGATCCGCC 4259
QY 4261 GCCTTATCGCTGTTTTCACCATTCAGATAGGCTCCGCAATTTGATTCCTTGAATTTTGTG 4320
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Db 4260 GCCTTATCGCTGTTTTCACCATTCAGATAGGCTCCGCAATTTGATTCCTTGAATTTTGTG 4319
QY 4321 GTATATTAACAAAACAAAGCTTAGTCAGATTCAAAACAAACATGCGTCTTACTAT 4380
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Db 4320 GTATATTAACAAAACAAAGCTTAGTCAGATTCAAAACAAACATGCGTCTTACTAT 4379
QY 4381 TCACCTCTGTTGTTCTTTGGCTTTGGCTTTGTTGAGCCAAAAGACAGACTATCAGT 4440
|||||
Db 4380 TCACCTCTGTTGTTCTTTGGCTTTGGCTTTGTTGAGCCAAAAGACAGACTATCAGT 4439
QY 4441 TCAAGGTCACACTATTTGTAATAGAAGAAATTCAGGMRAGTTACCTTTGGAGAA 4500
|||||
Db 4440 TCAAGGTCACACTATTTGTAATAGAAGAAATTCAGGMRAGTTACCTTTGGAGAA 4499
QY 4501 AGATCTCTGATTTTTCAGTCTTGTAGCTTGAAGCGCTTAAAGAGCTTAAAGAG 4560
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Db 4500 AGATCTCTGATTTTTCAGTCTTGTAGCTTGAAGCGCTTAAAGAGCTTAAAGAG 4559
QY 4561 CCTAAAATGAAGTTTCCACCTGTTTTCAAAAGAAAGCGAATTCGACACTTACAC 4620
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Db 4560 CCTAAAATGAAGTTTCCACCTGTTTTCAAAAGAAAGCGAATTCGACACTTACAC 4619
QY 4621 GAGATTTCTCAATTAATTTGTAATTTGTAATTCATATTCGCAACGCTCTTACAC 4680
|||||
Db 4620 GAGATTTCTCAATTAATTTGTAATTTGTAATTCATATTCGCAACGCTCTTACAC 4679
QY 4681 GAAATTTTCGATTTTTCAGCTTAAATAGATACCTGCTCGACAGCAAACTTTTG 4740
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Db 4680 GAAATTTTCGATTTTTCAGCTTAAATAGATACCTGCTCGACAGCAAACTTTTG 4739
QY 4741 TTAATTTCAAAAAGATGCGCTTAAAGAGTGTGTAAGTTCGTTGTTGC 4800
|||||
Db 4740 TTAATTTCAAAAAGATGCGCTTAAAGAGTGTGTAAGTTCGTTGTTGC 4799
QY 4801 GGACTTTTCATGATTTTTCGAGCTTTTTCATTAAGAAAATGTAATTTTATTTTAA 4860
|||||
Db 4800 GGACTTTTCATGATTTTTCGAGCTTTTTCATTAAGAAAATGTAATTTTATTTTAA 4859
QY 4861 AAATTTAATTTTACCGAATTCGCAAAAACAAATAGAGAACCGATTAATATTCGAG 4920
|||||
Db 4860 AAATTTAATTTTACCGAATTCGCAAAAACAAATAGAGAACCGATTAATATTCGAG 4919
QY 4921 CACATATGTTGAAATTAACGATCTTTTAAAGNCCATTTCTATATTTTACAC 4980
|||||
Db 4920 CACATATGTTGAAATTAACGATCTTTTAAAGNCCATTTCTATATTTTACAC 4979
QY 4981 AAATTTGCTGTGCGNCCGCGATCGTCATTTTGTATGCAAAATCAAGAAATTTGCAT 5040
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Db 4980 AAATTTGCTGTGCGNCCGCGATCGTCATTTTGTATGCAAAATCAAGAAATTTGCAT 5039
QY 5041 AATATTTCAAAAACCAATTAATGCGCAATTTCAAGCTTGAAGCAAAATTCAGAAAT 5100
|||||
Db 5040 AATATTTCAAAAACCAATTAATGCGCAATTTCAAGCTTGAAGCAAAATTCAGAAAT 5099
QY 5101 TCTAAAATTTAAAAAATATCATTCGAAATGTGAATTTGATTTCAACTTGAAGTCCAT 5160
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Db 5100 TCTAAAATTTAAAAAATATCATTCGAAATGTGAATTTGATTTCAACTTGAAGTCCAT 5159
QY 5161 ATGCCAAATTTGCTATTTCCGNNNTTGGANNAATTTTTCACGTGCGCCGAAAAGAG 5220
|||||
Db 5160 ATGCCAAATTTGCTATTTCCGNNNTTGGANNAATTTTTCACGTGCGCCGAAAAGAG 5219
QY 5221 AAAGCAGANNACGATTTTCGGCAATTTTTCCTGATACCGTGTCAATTAATTTGAAACTC 5280
|||||
Db 5220 AAAGCAGANNACGATTTTCGGCAATTTTTCCTGATACCGTGTCAATTAATTTGAAACTC 5279
QY 5281 TAATTAAGCTGTATTTTCTGTATTTGACACTAATCAATTAATTTGCAATTAATA 5340
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Db 5280 TAATTAAGCTGTATTTTCTGTATTTGACACTAATCAATTAATTTGCAATTAATA 5339
QY 5341 TATTAATTTGATGTTGCTGTAGAAAAAACCACAAACCTCATCTGCTTATGGC 5400
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Db 5340 TATTAATTTGATGTTGCTGTAGAAAAAACCACAAACCTCATCTGCTTATGGC 5399
QY 5401 TGCCATATATTTCTAGGACATATTAACAAACCTTAATTTCTGCAACACTACAGC 5460
|||||
Db 5400 TGCCATATATTTCTAGGACATATTAACAAACCTTAATTTCTGCAACACTACAGC 5459
QY 5461 TATCAACGTAATTTAGTATTTCAATTTTCAGTCCGACCCGATGACAGCTGCTCA 5520
|||||
Db 5460 TATCAACGTAATTTAGTATTTCAATTTTCAGTCCGACCCGATGACAGCTGCTCA 5519
QY 5521 TGCATATCAACAAAGAGAGATTTCTACCTTACCGATCCGACAGAGATCCCTCA 5580
|||||
Db 5520 TGCATATCAACAAAGAGAGATTTCTACCTTACCGATCCGACAGAGATCCCTCA 5579
QY 5581 TCTCTCCATACCTATATATCAACCAACAGTCAACGTAAGAGGCGGATGCAACGCTG 5640
|||||
Db 5580 TCTCTCCATACCTATATATCAACCAACAGTCAACGTAAGAGGCGGATGCAACGCTG 5639
QY 5641 TTTGAGATATTTATTTCCAAAGAGAGATGCTGAGACCTATGATATGACATATCTCA 5700
|||||
Db 5640 TTTGAGATATTTATTTCCAAAGAGAGATGCTGAGACCTATGATATGACATATCTCA 5699
QY 5701 CTCTTGATATTTCTTCCGCTTAAGACAAAGAGAGATGCTTAAGAAATGTTTTTGTGTT 5760
|||||
Db 5700 CTCTTGATATTTCTTCCGCTTAAGACAAAGAGAGATGCTTAAGAAATGTTTTTGTGTT 5759
QY 5761 GGTGTTGCTGTTTGAAGGAGAGACTTCTATCTCTTTAATTTCAACAAATTAATTTG 5820
|||||
Db 5760 GGTGTTGCTGTTTGAAGGAGAGACTTCTATCTCTTTAATTTCAACAAATTAATTTG 5819
QY 5821 GAAACCGTTGAATTTTAACTTTGAACGTAAGAAAGTTGCTGATTTGTTGCAAT 5880
|||||
Db 5820 GAAACCGTTGAATTTTAACTTTGAACGTAAGAAAGTTGCTGATTTGTTGCAAT 5879
QY 5881 TTTTCCAGATATATCTTTTGATATACAAATTAAGCAAGTCAAGCAGCAAAATTTAGC 5940
|||||
Db 5880 TTTTCCAGATATATCTTTTGATATACAAATTAAGCAAGTCAAGCAGCAAAATTTAGC 5939
QY 5941 GAAACACAAAATTAATAGAGATGCGCAACATTTTTCACCGCAAAATATCTCGTAGGAAA 6000
|||||
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Dh 1080 TGGATGCTCTCCGATTCATAGATACAGCGGTTGTATGATGCGCGAACCCTTCTGTC 1139
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Dh 1380 TTCAGATCTACAAATCGGAGATATCTGATCTGAGCTTTCGCTTCTTCTGCTCCCA 1439
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Db 6540 GTTTGATTAATTAATTTCA 6559

RESULT 5
US-60-360-039-29563
; Sequence 29563, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 29563
; LENGTH: 713
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-60-360-039-29563

Query Match 10.9%; Score 713; DB 80; Length 713;
Best Local Similarity 100.0%; Pred No. 1.1e-103;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 772 ATGATTAACATTCGACATGCTGATTTGCTGCGCTTGCGGCGAGATCGATTTCCCGC 831
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QY 832 TCCTTTGGAACATCGATCGTCAACAGAGTGGGATTTTGAATTTTCCGTAATTTG 891
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Db 361 CTTCGCTGCGAGAGATGAGATGCGAGTTTGGCGTTGCAATTCACCGCTTTTGAGAT 1251
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QY 1252 TTTCCCATCATTTTCCATCTCTTAACGAAATTCCTTTAGATTCGATTTGGCTAAG 1311
Db 481 TTTCCCATCATTTTCCATCTCTTAACGAAATTCCTTTAGATTCGATTTGGCTAAG 540
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Db 1312 GGAGTCATATATGTTGAGACAGTAGAGTTGAATTAATTAATTTTAAATTA 1371


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/ LENGTH: 1315 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 7..846
/ OTHER INFORMATION: /product= "Ced-9"
/ US-08-288-295-2

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Query Match
Best Local Similarity 9.6%; Score 632.6; DB 6; Length 1315;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 3393 GGAAGCTTATGATGACATGCGGAAACAAATGAAAGGACCTACGACGAGAGAGAGCTGA 3452
DB 669 GGAGCACTTCATGACACTGCGAAACAAATGAAAGGACCTACGACGAGAGAGAGCTGA 728
QY 3453 AAAAGTGGAGCGCGGAGACAGACAGACGAGTGTGATGATGGCGGTGGAGTAACAGC 3512
DB 729 AAAAGTGGAGCGCGGAGACAGACAGACGAGTGTGATGATGGCGGTGGAGTAACAGC 788
QY 3513 TGGAGCATTTGGAATGTTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 3572
DB 789 TGGAGCATTTGGAATGTTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 848
QY 3573 ACCTATTCATTTTGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3632
DB 849 ACCTATTCATTTTGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
QY 3633 TTTGCTCACTGATTCCTCATCTTTTGGACGTGAGAAAGTGGAGAAAGCTAGGCCACAAT 3692
DB 909 TTTGCTCACTGATTCCTCATCTTTTGGACGTGAGAAAGTGGAGAAAGCTAGGCCACAAT 968
QY 3693 TACGGCTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3752
DB 969 TACGGCTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028
QY 3753 GGCCAAACCTTACTGCGCGTAATATCACTTTTCCGTGTCATGATTCGTCACAAAA 3812
DB 1029 GGCCAAACCTTACTGCGCGTAATATCACTTTTCCGTGTCATGATTCGTCACAAAA 1088
QY 3813 CCCGTAACCTTACTTTTCCGCGTGGCTAGCCGCGGCTTCCGTCATGATTCGTCACAAAA 3872
DB 1089 CCCGTAACCTTACTTTTCCGCGTGGCTAGCCGCGGCTTCCGTCATGATTCGTCACAAAA 1148
QY 3873 AAGTACCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3932
DB 1149 AAGTACCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1208
QY 3933 TTCCAACTCCCGCAATTCCTAGCGGTAGCGGCTTGTGATTTATTTTCAAAAT 3992
DB 1209 TTCCAACTCCCGCAATTCCTAGCGGTAGCGGCTTGTGATTTATTTTCAAAAT 1268
QY 3993 GTTTTCTCTCTACAAACAAAAAAGCGTTC 4025
DB 1269 GTTTTCTCTCTACAAACAAAAAAGCGTTC 1301

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RESULT 8

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/ Sequence 4; Application US/08288295
/ GENERAL INFORMATION:
/ APPLICANT: Horvitz, H. Robert
/ APPLICANT: Hengartner, Michael
/ TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
/ TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: FISH & RICHARDSON
/ STREET: 225 Franklin Street, Suite 3100

```

```

/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A. (F) ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 5.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/288, 295
/ FILING DATE: 10-AUG-1994
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/927, 681
/ FILING DATE: 10-AUG-1992
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 01997/201003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELETYPE: 200154
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1315 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 7..846
/ OTHER INFORMATION: /product= "Ced-9"
/ US-08-288-295-4

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Query Match
Best Local Similarity 9.6%; Score 632.6; DB 6; Length 1315;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 3393 GGAAGCTTATGATGACATGCGGAAACAAATGAAAGGACCTACGACGAGAGAGCTGA 3452
DB 669 GGAGCACTTCATGACACTGCGAAACAAATGAAAGGACCTACGACGAGAGAGCTGA 728
QY 3453 AAAAGTGGAGCGCGGAGACAGACAGACGAGTGTGATGATGATGGCGGTGGAGTAACAGC 3512
DB 729 AAAAGTGGAGCGCGGAGACAGACAGACGAGTGTGATGATGATGGCGGTGGAGTAACAGC 788
QY 3513 TGGAGCATTTGGAATGTTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 3572
DB 789 TGGAGCATTTGGAATGTTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 848
QY 3573 ACCTATTCATTTTGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3632
DB 849 ACCTATTCATTTTGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
QY 3633 TTTGCTCACTGATTCCTCATCTTTTGGACGTGAGAAAGTGGAGAAAGCTAGGCCACAAT 3692
DB 909 TTTGCTCACTGATTCCTCATCTTTTGGACGTGAGAAAGTGGAGAAAGCTAGGCCACAAT 968
QY 3693 TACGGCTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3752
DB 969 TACGGCTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028
QY 3753 GGCCAAACCTTACTGCGCGTAATATCACTTTTCCGTGTCATGATTCGTCACAAAA 3812
DB 1029 GGCCAAACCTTACTGCGCGTAATATCACTTTTCCGTGTCATGATTCGTCACAAAA 1088
QY 3813 CCCGTAACCTTACTTTTCCGCGTGGCTAGCCGCGGCTTCCGTCATGATTCGTCACAAAA 3872
DB 1089 CCCGTAACCTTACTTTTCCGCGTGGCTAGCCGCGGCTTCCGTCATGATTCGTCACAAAA 1148

```


TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELE: 200154
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1315 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..846
 OTHER INFORMATION: /product= "Ced-9"

Query Match 9.6%; Score 632.6; DB 6; Length 1315;
 Best Local Similarity 99.8%; Pred. No. 8e-91;
 Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3393 GGACGACTTATGACACTCGGAAACAAATGAAAGAGACTACGAGAGAGAGAGCTGA 3452
 DB 669 GGACGACTTATGACACTCGGAAACAAATGAAAGAGAGACTACGAGAGAGAGCTGA 728
 QY 3453 AAAAGTGGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3512
 DB 729 AAAAGTGGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 788
 QY 3513 TGGAGCATTGGAATGTTGGAGTGTGTGTGGGAGATGATGATGATGATGATGATGAT 3572
 DB 789 TGGAGCATTGGAATGTTGGAGTGTGTGTGGGAGATGATGATGATGATGATGATGAT 848
 QY 3573 ACATATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3632
 DB 849 ACATATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 908
 QY 3633 TTTTGCTACTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 3692
 DB 909 TTTTGCTACTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 968
 QY 3693 TACGGCTCTGTGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 3752
 DB 969 TACGGCTCTGTGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 1028
 QY 3753 GGGCAAAACCTACTCGCGGTAATATCAACTTTCCGCTTCCTGATTCGATTCGATTCG 3812
 DB 1029 GGGCAAAACCTACTCGCGGTAATATCAACTTTCCGCTTCCTGATTCGATTCGATTCG 1088
 QY 3813 CCGTGAACCTACTTTTTCGCGGCTAGCCCTCCGCTTCCTGATTCGATTCGATTCGAT 3872
 DB 1089 CCGTGAACCTACTTTTTCGCGGCTAGCCCTCCGCTTCCTGATTCGATTCGATTCGAT 1148
 QY 3873 AAGTACCCCTGATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3932
 DB 1149 AAGTACCCCTGATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1208
 QY 3933 TTCCAACTCCCGCAAAATTCCTGTACGCGATTCGATTCGATTCGATTCGATTCGAT 3992
 DB 1209 TTCCAACTCCCGCAAAATTCCTGTACGCGATTCGATTCGATTCGATTCGATTCGAT 1268
 QY 3993 GTTTTCTCTACACAAACAAAAGCGTTC 4025
 DB 1269 GTTTTCTCTACACAAACAAAAGCGTTC 1301

RESULT 11
 ; Sequence 2, Application us/08801248
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, H. Robert
 ; APPLICANT: Hengartner, Michael
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED

TITLE OF INVENTION: CELL DEATH AND USES THEREFOR
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & RICHARDSON
 STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,248
 FILING DATE: 19-FEB-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/288,295
 FILING DATE: 10-AUG-1994
 APPLICATION NUMBER: US 07/927,681
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 01997/201003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELE: 200154
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1315 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..846
 OTHER INFORMATION: /product= "Ced-9"

Query Match 9.6%; Score 632.6; DB 12; Length 1315;
 Best Local Similarity 99.8%; Pred. No. 8e-91;
 Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3393 GGACGACTTATGACACTCGGAAACAAATGAAAGAGAGACTACGAGAGAGAGAGCTGA 3452
 DB 669 GGACGACTTATGACACTCGGAAACAAATGAAAGAGAGACTACGAGAGAGAGAGCTGA 728
 QY 3453 AAAAGTGGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3512
 DB 729 AAAAGTGGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 788
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 DB 789 TGGAGCATTGGAATGTTGGAGTGTGTGTGGGAGATGATGATGATGATGATGATGAT 848
 QY 3573 ACATATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3632
 DB 849 ACATATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 908
 QY 3633 TTTTGCTACTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 3692
 DB 909 TTTTGCTACTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 968
 QY 3693 TACGGCTCTGTGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 3752
 DB 969 TACGGCTCTGTGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 1028

Thu Mar 6 08:14:02 2003

us-09-993-420a-1.rnp

Page 22

[illegible]

RESULT 15
US-09-993-420A-2
: Sequence 2, Application US/09993420A

1 GENEKAT: Horvitz, H. Robert
 2 APPLICANT: Hengartner, Michael
 3 TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 4 TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
 5 TITLE OF INVENTION: USES THEREOF
 6 FILE REFERENCE: 01997/201006
 7 CURRENT APPLICATION NUMBER: US/09/993,420A

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1 FILE REFERENCE: 09/99/3,420A
2 CURRENT APPLICATION NUMBER: US-09/993,420A
3 CURRENT FILING DATE: 5001-11-09
4 PRIOR APPLICATION NUMBER: 09/234,166
5 PRIOR FILING DATE: 1999-01-20
6 PRIOR APPLICATION NUMBER: 07/898,933
7 PRIOR FILING DATE: 1992-06-12
8 PRIOR APPLICATION NUMBER: 07/927,681
9 PRIOR FILING DATE: 1992-08-10
10 PRIOR APPLICATION NUMBER: 08/288,295
11 PRIOR FILING DATE: 1994-08-10
12 PRIOR APPLICATION NUMBER: 08/601,248
13 PRIOR FILING DATE: 1997-02-19
14 NUMBER OF SEQ ID NOS: 8
15 SOFTWARE: FastSeq for Windows Version 4.0
16 SEQ ID NO 2
17 LENGTH: 1315
18 TYPE: DNA
19 ORGANISM: Caenorhabditis elegans
20 FEATURE:
21 NAME/KEY: CDS
22 LOCATION: (7)...(846)
23 US-09-993-420A-2

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Query Match	9.6%;	Score 632.6;	DB 37;	Length 1315;
Best Local Similarity	99.8%;	Pred. No. 8e-91;		
Matches 632;	Conservative	1;	Mismatches	0;
			Indels	Gaps
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[illegible]

Search completed: February 28, 2003, 08:42:54
Job time : 12517.6 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 18:35:25 : Search time 1185.38 Seconds
(Without alignments)
12462.745 Million cell updates/sec

Title: US-09-993-420a-1

Perfect score: 6560

Sequence: 1 atcgatagtcgtcaccaat.....gtttgataaataatcaaa 6560

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapept 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6535.4	99.6	6560	AA054629	Genomic region con
2	631	9.6	1315	AA054630	ced-9 coding seque
3	139.2	2.1	7653	AA054630	Nematode Ced-3 gen
4	139.2	2.1	7653	AA054630	Nematode Ced-3 gen
5	137.6	2.1	7653	AA064736	ced-3 (G2487A) gen
6	137.6	2.1	7653	AA064736	ced-3 (G2487A) gen
7	137.6	2.1	7653	AA064736	ced-3 (G5757A) gen
8	137.6	2.1	7653	AA064736	ced-3 (C5940T) gen
9	137.6	2.1	7653	AA064736	ced-3 (G6297A) gen
				AA064740	ced-3 (C6322T) gen

C 10	137.6	2.1	7653	15	AA064741	ced-3 (G6372A) gen
C 11	137.6	2.1	7653	15	AA064742	ced-3 (C6434T) gen
C 12	137.6	2.1	7653	15	AA064743	ced-3 (C6485T) gen
C 13	137.6	2.1	7653	15	AA064744	ced-3 (G6536A) gen
C 14	137.6	2.1	7653	15	AA064745	ced-3 (C7020T) gen
C 15	137.6	2.1	7653	15	AA054401	ced-3 gene. Caeno
C 16	137.6	2.1	7653	15	AA054466	ced-3 gene. Caeno
C 17	122.8	1.9	6560	15	AA054629	Genomic region con
C 18	121	1.8	42521	20	AA232013	Human MTH1 relate
C 19	121	1.8	42521	22	AA232013	Human MTH1 relate
C 20	116.8	1.8	42521	22	AA232013	Human MTH1 relate
C 21	116.8	1.8	42521	22	AA232013	Human MTH1 relate
C 22	102.2	1.6	6612	21	AA064963	C. elegans sarco/e
C 23	102.2	1.6	6612	21	AA064963	C. elegans sarco/e
C 24	102.2	1.6	11207	21	AA064960	DNA fragment of up
C 25	102.2	1.6	11207	21	AA064960	C. elegans sarco/e
C 26	101.8	1.6	7653	17	AA064960	Cosmid K119 conta
C 27	101.8	1.6	7653	21	AA064960	Nematode Ced-3 gen
C 28	100.6	1.5	6612	21	AA064963	ced-3 gene. Caeno
C 29	100.6	1.5	6612	21	AA064963	C. elegans sarco/e
C 30	100.6	1.5	11207	21	AA064960	DNA fragment of up
C 31	100.6	1.5	11207	21	AA064960	C. elegans sarco/e
C 32	100.2	1.5	7653	15	AA064736	Cosmid K119 conta
C 33	100.2	1.5	7653	15	AA064736	ced-3 (G2487A) gen
C 34	100.2	1.5	7653	15	AA064736	ced-3 (G5757A) gen
C 35	100.2	1.5	7653	15	AA064736	ced-3 (C5940T) gen
C 36	100.2	1.5	7653	15	AA064736	ced-3 (G6297A) gen
C 37	100.2	1.5	7653	15	AA064740	ced-3 (G6372T) gen
C 38	100.2	1.5	7653	15	AA064741	ced-3 (G6372T) gen
C 39	100.2	1.5	7653	15	AA064742	ced-3 (G6434T) gen
C 40	100.2	1.5	7653	15	AA064744	ced-3 (G6485T) gen
C 41	100.2	1.5	7653	15	AA064745	ced-3 (G6536A) gen
C 42	100.2	1.5	7653	15	AA064745	ced-3 (C7020T) gen
C 43	98.6	1.5	7653	15	AA054401	ced-3 gene. Caeno
C 44	93	1.4	4560	21	AA037888	ced-3 gene. Caeno
C 45	93	1.4	4560	24	ABK48340	C. elegans PAMP co

ALIGNMENTS

RESULT 1
ID AA054629 standard; DNA: 6560 BP.
AA054629;
23-JUN-1994 (first entry)
Genomic region containing ced-9 gene.
Cell death: senescence; programmed cell death; ced-9; myocardial
infarction; stroke; brain injury; neurodegenerative disease;
muscular degenerative disease; ageing; hypoxia; ischemia; toxemia;
infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;
oncogene; ss.
Caenorhabditis elegans.
WO9325683-A.
23-DEC-1993.
14-JUN-1993; 93WO-US05651.
12-JUN-1992; 92US-0898933.
10-AUG-1992; 92US-0927681.
(MASI) MASSACHUSETTS INST TECHNOLOGY.
Hengartner M, Horvitz HR.
WPI: 1994-007540/01.

XX Caenorhabditis elegans cell death-protective gene - used to
 PT develop agents for preventing cell death or for reducing
 PT population of cells
 XX

XX Claim 3; page 54-58; 112pp; English.

XX
 CC ced-9 is essential for C. elegans development and apparently
 CC functions by protecting cells during development from programmed
 CC cell death. ced-9 was shown to function by antagonising the
 CC activities of cell death genes ced-3 and ced-4. The protein product
 CC of the human oncogene bcl-2 was found to have a similar sequence
 CC to the ced-9 protein. The ced-9 gene can be used for developing
 CC agents for treating a condition characterised by increased cell death
 CC such as myocardial infarction, stroke, traumatic brain injury,
 CC neurodegenerative disease, muscular degenerative disease, ageing,
 CC hypoxia, ischaemia, toxemia, infection or hair loss. It can also
 CC be used for reducing a population of cells in the treatment of
 CC neoplastic growth cancerous tissue, infected cells or autoreactive
 CC immune cells.
 XX

SQ Sequence 6560 BP; 2040 A; 1274 C; 1203 G; 2023 T; 20 other:

Query Match 99.6%; Score 6535.4; DB 15; Length 6560.
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 6556; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 DB 1 ATCGATAGTCGTACCAATGATTTTCGATTTCTCACTAGTCCTGCTCACAATTGA 60
 QY 61 CAAATATCGAGAAAGAAAGATGCAAGAGATGAGAGATTCGCAATCTAATATTT 120
 DB 61 CAAATATCGAGAAAGAAAGATGCAAGAGATGAGAGATTCGCAATCTAATATTT 120
 QY 121 TAAATTTAAAAATTCATTTTCGAATTCGAATTCACCTCTACTGTTTGAATATCCAA 180
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 QY 361 CTGTCCTTTGAGAGCAACCAATCTTAAAGCTGTCCAGCAGAGAGTCCACTCGCCA 420
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 DB 481 GGATCAGAAATTCGAGAAATTTAGATTTCATCTTGAATTTGCAATGGAAAAATATTT 540
 QY 541 ATTCAAGAAATTCAGAGAAATTCAGAAAAAACAACAAAAAGAACAAAAACAAGTC 600
 DB 541 ATTCAAGAAATTCAGAGAAATTCAGAAAAAACAACAAAAAGAACAAAAACAAGTC 600
 QY 601 GAAAGATCGCCGCGGCTGTTGCTGAGCATCTCTTCAAGCAGAGCGCTGCTGCGC 660
 DB 601 GAAAGATCGCCGCGGCTGTTGCTGAGCATCTCTTCAAGCAGAGCGCTGCTGCGC 660
 QY 661 ACTTCTGCGCTGCTGCTGCTATTTCCGACAAATTCACACTGTTTGAACGCA 720
 DB 661 ACTTCTGCGCTGCTGCTGCTATTTCCGACAAATTCACACTGTTTGAACGCA 720

DB 661 ACTTCTGCGCTGCTGCTGCTATTTCCGACAAATTCACACTGTTTGAACGCA 720
 QY 721 CCGGCCGTTTCTTTTTCATTTTGAAGAAATCAGCATGTTTTCAGAGATTAAC 780
 DB 721 CCGGCCGTTTCTTTTTCATTTTGAAGAAATCAGCATGTTTTCAGAGATTAAC 780
 QY 781 ATTCCAACTGCGATTTGTCGCGCTGCGGCGCAGATGTCGATTTCCGCTCTTGGCA 840
 DB 781 ATTCCAACTGCGATTTGTCGCGCTGCGGCGCAGATGTCGATTTCCGCTCTTGGCA 840
 QY 841 ACATGATGTCGTCACCAAGGCGGATTTTGAATTTTCCGGAATTTGATTTT 900
 DB 841 ACATGATGTCGTCACCAAGGCGGATTTTGAATTTTCCGGAATTTGATTTT 900
 QY 901 TGTGTAGCATGAAGGAGAAATGATTAACAGACATCTTTTCAATTAATTAATA 960
 DB 901 TGTGTAGCATGAAGGAGAAATGATTAACAGACATCTTTTCAATTAATTAATA 960
 QY 961 TATTCAGATTCGAGCAAGAGCCCAATCCAGAGTTGCGATGGGAATACCTGTTGAAG 1020
 DB 961 TATTCAGATTCGAGCAAGAGCCCAATCCAGAGTTGCGATGGGAATACCTGTTGAAG 1020
 QY 1021 CAGGCTCCAGAAATTCGCGCATGCTTCACATCTCACCGCTTACAGCCACATTTGACC 1080
 DB 1021 CAGGCTCCAGAAATTCGCGCATGCTTCACATCTCACCGCTTACAGCCACATTTGACC 1080
 QY 1081 TGSATGCTCTCCGGAATTCATAGATCAGCGGTTGTATGCGCGGAGACCTTCTGTC 1140
 DB 1081 TGSATGCTCTCCGGAATTCATAGATCAGCGGTTGTATGCGCGGAGACCTTCTGTC 1140
 QY 1141 GGAGGAATGCGATTCGCGAGTTTGGCGCTTGCATCCCGCTTTGGAGATTCATCGT 1200
 DB 1141 GGAGGAATGCGATTCGCGAGTTTGGCGCTTGCATCCCGCTTTGGAGATTCATCGT 1200
 QY 1201 AGCTGGAATTCACATGCGCGGCTGACGCGTCTTCAAGTACATCATTTGCTTCCCATC 1260
 DB 1201 AGCTGGAATTCACATGCGCGGCTGACGCGTCTTCAAGTACATCATTTGCTTCCCATC 1260
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 DB 1261 AATTTTCATACCTTTAAGCAATTCGCTTTAGAGATTCGATTTGGCGTAAGGGAGTCAAT 1320
 QY 1321 AATGTTGCAAGAGTATGGAATTTAATTAATTAATTAATTAATTAATTAATTAAT 1380
 DB 1321 AATGTTGCAAGAGTATGGAATTTAATTAATTAATTAATTAATTAATTAATTAAT 1380
 QY 1381 TTTCAGATCTACAAATCGGGAATATCTGATCTGACCTTTGCGTAATTTCTCTCGCCA 1440
 DB 1381 TTTCAGATCTACAAATCGGGAATATCTGATCTGACCTTTGCGTAATTTCTCTCGCCA 1440
 QY 1441 TTGCTCTCACTCTTTCGCAAGAACAGACACAGACTGCTTAGGCACAGATGCTCGGCC 1500
 DB 1441 TTGCTCTCACTCTTTCGCAAGAACAGACACAGACTGCTTAGGCACAGATGCTCGGCC 1500
 QY 1501 TTCTTTTCTTACGCGCCGCGCCAGCTGACAAATTTCTGCAATTTTCAATTTTACCGTTG 1560
 DB 1501 TTCTTTTCTTACGCGCCGCGCCAGCTGACAAATTTCTGCAATTTTCAATTTTACCGTTG 1560
 QY 1561 AATTTCTGATTTCTCTCTTTTCCGATTAATTTTACCTCTCTCTCTCTCTCTCTCTCT 1620
 DB 1561 AATTTCTGATTTCTCTCTTTTCCGATTAATTTTACCTCTCTCTCTCTCTCTCTCTCT 1620
 QY 1621 GTCTAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1680
 DB 1621 GTCTAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1680
 QY 1681 GCGGCAACTGCTGAGCAATCGGCGGTAATGCGGCGCAAGATGCGCATGCGCAGATG 1740
 DB 1681 GCGGCAACTGCTGAGCAATCGGCGGTAATGCGGCGCAAGATGCGCATGCGCAGATG 1740
 QY 1741 AAGGATTTCTGGGATTAAGAGCAACAGAGCCACAGATTTTGAATGATGATGCT 1800
 DB 1741 AAGGATTTCTGGGATTAAGAGCAACAGAGCCACAGATTTTGAATGATGATGCT 1800

QY 1801 CAGACTTCCATCAGCAGATGAGCAGCTTCGACCGGAGAAATGTCATCGAGAGTCA 1860
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Db 1801 CAGACTTCCATCAGCAGATGAGCAGCTTCGACCGGAGAAATGTCATCGAGAGTCA 1860
QY 1861 ATTGATGAAAAATCAATGATGAGGAGAGAGCCAGGCTTGATATCGAGGATTTGGTGA 1920
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Db 1861 ATTGATGAAAAATCAATGATGAGGAGAGAGCCAGGCTTGATATCGAGGATTTGGTGA 1920
QY 1921 ATTTTAAATTTTAAATTTAAATTTTCTGCTGCTTCAGTGCATTTTCAAG 1980
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Db 1921 ATTTTAAATTTTAAATTTTAAATTTTCTGCTGCTTCAGTGCATTTTCAAG 1980
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Db 1981 CACCGAATCCGCAAAAACGGAATGGAATGTTGAGACCGGGAGTCCGCTGAGAGTG 2040
QY 2041 CAACCGGAGCAGAAATGATGAGATGATGAGAGATTCGAGAGAGAGAGAGAGAGAGAG 2100
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Db 2041 CAACCGGAGCAGAAATGATGAGATGATGAGAGATTCGAGAGAGAGAGAGAGAGAGAG 2100
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Db 2221 CGTTGGTAAAGGAGAAATCTGAAAAAAGTTGCAAAAATTCGAAAAATTCGCCGAA 2280
QY 2281 AGGTGGCAAAAAAATCATTGCAAAATTTGTTTCTCTGAGAAATCAGCAAAATC 2340
| | | | |
Db 2281 AGGTGGCAAAAAAATCATTGCAAAATTTGTTTCTCTGAGAAATCAGCAAAATC 2340
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Db 2761 GGTCTAATCTGTTGGGGGTTTCTAGCTGCAAAATGATGAGATCCGAGAGCTGAG 2820
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QY 2881 AACTGGAAGGAGACATATCGGAGCTGGGTTAGAGATTTTGGATAGACATTTAGAGTCAA 2940
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| | | | |
Db 2941 TATCCCTTTCCTTGTATCCTTGTGACTTCCGGGGTGTGTAAGCCGATTAATTACAG 3000
QY 3001 GTTCGGTACGCTTGTGGGGGAGAGCTGGAACATATTCAGATATTTACTGTTATGAT 3060
| | | | |
Db 3001 GTTCGGTACGCTTGTGGGGGAGAGCTGGAACATATTCAGATATTTACTGTTATGAT 3060
QY 3061 AATGTTATTTGTTTACGGAATTTACAAAAATTCGAGATTCGATTTTCAACATTTTGAAG 3120
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QY 3121 GCAAAATATCAGTACAGAAAACTACGTAATTTCTTAAATTTTAAATTTTACAAAT 3180
| | | | |
Db 3121 GCAAAATATCAGTACAGAAAACTACGTAATTTCTTAAATTTTAAATTTTACAAAT 3180
QY 3181 AAGAAATATACCACTAATCAAAAAAATTTAATTCAAAAAATGAGCCGTAATTCAGT 3240
| | | | |
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Db 3241 ACAGTAGCATTTAAAGATTTACTGATTTTCTGCTACGAGATTTTCCGCTCAATAT 3300
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QY 3361 TGTGAATTAATAAATAATCAAGAAAAAATTCAGAGACACTTCAATGACCTGGAACAA 3420
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QY 3421 ATGAAGAGGACTGCAAG 3480
| | | | |
Db 3421 ATGAAGAGGACTGCAAG 3480
QY 3481 CGGTGCTGATGATTTGGCGCTGAGATTAACAGCTGAGAGCATTGGAATGCTGAGTGC 3540
| | | | |
Db 3481 CGGTGCTGATGATTTGGCGCTGAGATTAACAGCTGAGAGCATTGGAATGCTGAGTGC 3540
QY 3541 GTGTGTTGGGGGATGATTTGACCTTACGTTAAGTAACGTAATTTGTGTAATTAAT 3600
| | | | |
Db 3541 GTGTGTTGGGGGATGATTTGACCTTACGTTAAGTAACGTAATTTGTGTAATTAAT 3600
QY 3601 TTATGTACAACTCTTACATTTGAATCTCATTTTGTGCTACGATTTCTCTGATTTGA 3660
| | | | |
Db 3601 TTATGTACAACTCTTACATTTGAATCTCATTTTGTGCTACGATTTCTCTGATTTGA 3660
QY 3661 ACTGGAAGAGTGGGAAACCTAGGCGCACAAATTTAGCGCTCTGTGCTGATTTGAGATT 3720
| | | | |
Db 3661 ACTGGAAGAGTGGGAAACCTAGGCGCACAAATTTAGCGCTCTGTGCTGATTTGAGATT 3720
QY 3721 TACTGCAATTTTTCGATTTGCTTTTGTGCGCAAAACCTACTTCCGCTAATATCA 3780
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Db 3721 TACTGCAATTTTTCGATTTGCTTTTGTGCGCAAAACCTACTTCCGCTAATATCA 3780
QY 3781 ACTTTTCGCTGTTCTGATTTGCTCAAAAAACCTGAAACCTTACTTTCTGCGCTG 3840
| | | | |
Db 3781 ACTTTTCGCTGTTCTGATTTGCTCAAAAAACCTGAAACCTTACTTTCTGCGCTG 3840
QY 3841 GCTTACGCTCCGCTCTCTTCCACATTTGCAAAAGTACCCCTGATTCGAATTAATATC 3900
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Db 3841 GCTTACGCTCCGCTCTCTTCCACATTTGCAAAAGTACCCCTGATTCGAATTAATATC 3900
QY 3901 TTTCACTTTAATCTCTCTTTCTGTTGCGCTTCTCAACTCCGCCAAATTTCTGTAAG 3960
| | | | |
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QY 3961 GTACGCACTTTGATTAATTTTCTCTCTGTAACAAACAAAAAATC 4020

|||||
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Oy 4021 GGTCTTTTATTCACCCCTTTTGGAAAGCAAGTCATTTTGTATTAATAGCGTGGC 4080
Db 4021 GGTCTTTTATTCACCCCTTTTGGAAAGCAAGTCATTTTGTATTAATAGCGTGGC 4080
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Db 4141 TCATTTTATTAATTAATGATTCATTTCTTCGCTCTCTCTCTCTCGAGACGAGTCAT 4200
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Db 4201 TCGATGCGCTTGAATTTTTCGAAAAACAAATTTTGTGTAGTAAACGATCCGCC 4260
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Db 4261 GCGTATCGCGTTCACATTCAGATAGCGCTCGCATTTGATTCCTGAAATTTGTG 4320
Oy 4321 GTATATTAACAAAAACGTTAGTCACGATTCAAAAACAAATCGCGTCTTACTAT 4380
Db 4321 GTATATTAACAAAAACGTTAGTCACGATTCAAAAACAAATCGCGTCTTACTAT 4380
Oy 4381 TCACCTCTGTTCTTCTTGGCTTGGCTTGTGTAGGCAAGACAGACTATCACTG 4440
Db 4381 TCACCTCTGTTCTTCTTGGCTTGGCTTGTGTAGGCAAGACAGACTATCACTG 4440
Oy 4441 TCAAGGATCACTATTTGTATTAAGAGAGATTCAGGMRAGTTACCTTGGGAGAA 4500
Db 4441 TCAAGGATCACTATTTGTATTAAGAGAGATTCAGGMRAGTTACCTTGGGAGAA 4500
Oy 4501 AGATCTCTGAGTTTTCAGTCTTGTAGTTGAAACGCTTAAAGAGATTAAGAG 4560
Db 4501 AGATCTCTGAGTTTTCAGTCTTGTAGTTGAAACGCTTAAAGAGATTAAGAG 4560
Oy 4561 CCTAAATTAAGATTTTCCACCTGTTTCAAAAGAAAGCCGAATTTGACACCTTAC 4620
Db 4561 CCTAAATTAAGATTTTCCACCTGTTTCAAAAGAAAGCCGAATTTGACACCTTAC 4620
Oy 4621 GAGATTTTCATTAATTTTATTTGAAATTTTCATTCATCCCAACGTTCTTACAC 4680
Db 4621 GAGATTTTCATTAATTTTATTTGAAATTTTCATTCATCCCAACGTTCTTACAC 4680
Oy 4681 GAAATTTGAGATTTTGAAGCTTAATAATGATACCTGCTCGACAGAAACATTTTG 4740
Db 4681 GAAATTTGAGATTTTGAAGCTTAATAATGATACCTGCTCGACAGAAACATTTTG 4740
Oy 4741 TTAATTCACAAAGATGCGCTTAAAGAGCTGTAGTTGAAACCTGCTGTTG 4800
Db 4741 TTAATTCACAAAGATGCGCTTAAAGAGCTGTAGTTGAAACCTGCTGTTG 4800
Oy 4801 GAGCTTTTCATCGATTTTGTAGCGTTTATTAAGAAAAATGATTAATTTACAA 4860
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Oy 4861 AAATTTAATTTTACGATCGCAAAACAAATTAAGAAACCGGATTAATAATTCGAC 4920
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Db 4921 CAACAATTAATTTGAAATTTAGAGTCTTTTAAGNGNCCATTTCTATTTTCACAC 4980
Oy 4981 AAATCTGCTGCTGNNCCGATGATGATTTTGTATGAGAAATGAAAGAAATTCAT 5040
Db 4981 AAATCTGCTGCTGNNCCGATGATGATTTTGTATGAGAAATGAAAGAAATTCAT 5040
Oy 5041 ATATGTTCAAAAAACCAATTAATGAGGATTTCAAGCTTGAACGAAATTCAGAAAT 5100
Db 5041 ATATGTTCAAAAAACCAATTAATGAGGATTTCAAGCTTGAACGAAATTCAGAAAT 5100

Db 5041 ATATGTTCAAAAAACCAATTAATGAGGATTTCAAGCTTGAACGAAATTCAGAAAT 5100
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Db 5101 TCTAAAAATTAATTAATTTTCGAAATGTAATTTGATTTGATTTGATTTGATTTG 5160
Oy 5161 ATGCAATTTTCGCTTTCGNNNTTCGANNATTTTGTTCACGCTGCGCGCAAAAGAG 5220
Db 5161 ATGCAATTTTCGCTTTCGNNNTTCGANNATTTTGTTCACGCTGCGCGCAAAAGAG 5220
Oy 5221 AAAGACGANNAGTATTTTTCGCAATTTTTCGTAACCGTGCATTTATTTGAACCTG 5280
Db 5221 AAAGACGANNAGTATTTTTCGCAATTTTTCGTAACCGTGCATTTATTTGAACCTG 5280
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Oy 5641 TTTGAGATTTGATTTCCAAAGAGAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5700
Db 5641 TTTGAGATTTGATTTCCAAAGAGAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5700
Oy 5701 CTCTGATATTTCTTCGCTTAAGACAAAGAGAGTCTTAAGAAATGTTTTTGTGTT 5760
Db 5701 CTCTGATATTTCTTCGCTTAAGACAAAGAGAGTCTTAAGAAATGTTTTTGTGTT 5760
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Db 5821 GAAACGTTGAATTTTAACTTGAACCTGTAAGAAAGTTGCTGATTAATTTGACAT 5880
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Db 5881 TTTGCAAGTATTTCTTGTGATATTCACATTAACCAAGTCAAGCAAGCAATTTACG 5940
Oy 5941 GAAACGAAATTAATTAAGAGATGCGCAACATTTTGAACCGCAAAATTTCTGCGCAA 6000
Db 5941 GAAACGAAATTAATTAAGAGATGCGCAACATTTTGAACCGCAAAATTTCTGCGCAA 6000
Oy 6001 CTACGATATTTCTTAAGAGATGCTGTAAGAGGATTTGACCGCAAAATTTCTGCGCAA 6060
Db 6001 CTACGATATTTCTTAAGAGATGCTGTAAGAGGATTTGACCGCAAAATTTCTGCGCAA 6060
Oy 6061 AAATGATTAAGATTTGAAGAGATGCTGTAAGAGGATTTGACCGCAAAATTTCTGCGCAA 6120
Db 6061 AAATGATTAAGATTTGAAGAGATGCTGTAAGAGGATTTGACCGCAAAATTTCTGCGCAA 6120
Oy 6121 AAATGATTAAGATTTGAAGAGATGCTGTAAGAGGATTTGACCGCAAAATTTCTGCGCAA 6180
Db 6121 AAATGATTAAGATTTGAAGAGATGCTGTAAGAGGATTTGACCGCAAAATTTCTGCGCAA 6180

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OY 6181 ATATTTGNGNGTCAAATATGTTGNCACATACGATCCTCAGATTGTTGTTCTGTA 6240
DB 6181 ATATTTGNGNGTCAAATATGTTGNCACATACGATCCTCAGATTGTTGTTCTGTA 6240
OY 6241 TGTCTTGAAATTTTCCATTTCACATCAAAATAGCAAAATCTTAAATGTTGGTCTGCA 6300
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DB 6301 GGCACACATATGCTGATGTCGCGCAACACACACACAACTACGTTCTTTAA 6360
OY 6361 CAATATCATTTTAAATATGATATGATATTAATAATTTGCTAGACGCTAGGCTGCTT 6420
DB 6361 CAATATCATTTTAAATATGATATGATATTAATAATTTGCTAGACGCTAGGCTGCTT 6420
OY 6421 TTTTCAGTCGACAACTCTTAATTTAATGCGGGGCTCTCAAAAAGTCTTTCTTGAAA 6480
DB 6421 TTTTCAGTCGACAACTCTTAATTTAATGCGGGGCTCTCAAAAAGTCTTTCTTGAAA 6480
OY 6481 TATTAAGCTTTATATATATATATATTAATAATTTGATATCATATCAAAAGGACATA 6540
DB 6481 TATTAAGCTTTATATATATATATATTAATAATTTGATATCATATCAAAAGGACATA 6540
OY 6541 GTTTGATATTAATATATCA 6560
DB 6541 GTTTGATATTAATATATCA 6560

RESULT 2
AA054630
ID AA054630 standard; cDNA to mRNA; 1315 BP.
XX
AC AA054630;
XX
DT 23-JUN-1994 (first entry)
XX
DE ced-9 coding sequence.
XX
KM Cell death; senescence; programmed cell death; ced-9; myocardial
KM infarction; stroke; brain injury; neurodegenerative disease;
KM muscular degenerative disease; ageing; hypoxia; ischaemia; toxemia;
KM infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;
KM oncogene; ss.
XX
OS Caenorhabditis elegans.
XX
FH Key Location/Qualifiers
FT CDS 7..846
FT /*tag= a
FT /product= Ced-9.
XX
XX W09325683-A.
XX
XX 23-DEC-1993.
XX
XX 14-JUN-1993; 93MO-US05651.
XX
XX 12-JUN-1992; 92US-0898933.
XX
XX 10-AUG-1992; 92US-0927681.
XX
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Hengartner M, Horvitz HR.
XX
XX WPI; 1994-007540/01.
XX
XX P-PSDB; AAR47343.
XX
XX Caenorhabditis elegans cell death-protective gene - used to
XX PT develop agents for preventing cell death or for reducing
XX PT population of cells
XX

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PS Claim 3; Page 58-59; 112pp; English.
XX
XX ced-9 is essential for C. elegans development and apparently
CC functions by protecting cells during development from programmed
CC cell death. ced-9 was shown to function by antagonising the
CC activities of cell death genes ced-3 and ced-4. The protein product
CC of the human oncogene bcl-2 was found to have a similar sequence
CC to the ced-9 protein. The ced-9 gene can be used for developing
CC agents for treating a condition characterised by increased cell death
CC such as myocardial infarction, stroke, traumatic brain injury,
CC neurodegenerative disease, muscular degenerative disease, ageing,
CC hypoxia, ischaemia, toxemia, infection or hair loss. It can also
CC be used for reducing a population of cells in the treatment of
CC neoplastic growth cancerous tissue, infected cells or autoreactive
CC immune cells.
XX
SQ Sequence 1315 BP; 362 A; 290 C; 315 G; 347 T; 1 other;
Query Match 9.6%; Score 631; DB 15; Length 1315;
Best Local Similarity 99.7%; Pred. No. 9,8e-123;
Matches 631; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 3393 GGAGACTTTCATGACACTCGGAAACAAATGAAGAGACTACGAAGCAGACAGCTGA 3452
DB 669 GGAGACTTTCATGACACTCGGAAACAAATGAAGAGACTACGAAGCAGACAGCTGA 728
OY 3453 AAAAGTGGAGCGCCGGAAGCAGACAGCGGTGCTGATGATTTGGCGTGGAGTAACAGC 3512
DB 729 AAAAGTGGAGCGCCGGAAGCAGACAGCGGTGCTGATGATTTGGCGTGGAGTAACAGC 788
OY 3513 TGGAGCATTGGAATCTTTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3572
DB 789 TGGAGCATTGGAATCTTTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848
OY 3573 ACGTATTCATTTGCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3632
DB 849 ACGTATTCATTTGCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 908
OY 3633 TTTGCTACATGATTTCTCTATCTTTGACTGGAAGAGTGGAAAGCTAGGCCCAAT 3692
DB 909 TTTGCTACATGATTTCTCTATCTTTGACTGGAAGAGTGGAAAGCTAGGCCCAAT 968
OY 3693 TAGGGCTCTCTGCTGATTTACATTTTACATTTTACATTTTACATTTTACATTTTACAT 3752
DB 969 TAGGGCTCTCTGCTGATTTACATTTTACATTTTACATTTTACATTTTACATTTTACAT 1028
OY 3753 GGCCAAACCCCTACTCCGCGTAATATCAACTTTCCGCTGCTGATTTGCTCAAAA 3812
DB 1029 GGCCAAACCCCTACTCCGCGTAATATCAACTTTCCGCTGCTGATTTGCTCAAAA 1088
OY 3813 CCTGAAACCCCTAACTTTTCCGCGTGGCTAGCTCCGCTTCTCTTCCACATTTTCCA 3872
DB 1089 CCTGAAACCCCTAACTTTTCCGCGTGGCTAGCTCCGCTTCTCTTCCACATTTTCCA 1148
OY 3873 AAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3932
DB 1149 AAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1208
OY 3933 TTCCAACTCCCGCCAAATTTCTGACGCTACGCACTTTGATTTATTTTTCAAAT 3992
DB 1209 TTCCAACTCCCGCCAAATTTCTGACGCTACGCACTTTGATTTATTTTTCAAAT 1268
OY 3993 GTTTCTCTCTACACACAAACAAACGCTC 4025
DB 1269 GTTTCTCTCTACACACAAACAAACGCTC 1301

RESULT 3
AAT38196/C
ID AAT38196 standard; DNA; 7653 BP.
XX
XX AAT38196;
XX

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CC In plasmid pJ107 was sequenced. EMS-induced alleles were also
 CC sequenced. The gene codes for a cell death protein (AA98754) that
 CC is structurally similar to human interleukin-1 beta converting
 CC enzyme (ICE) (AA98755), suggesting that Ced-3 protein may be a
 CC cysteine protease like ICE and that ICE may be a human equivalent
 CC of the nematode cell death gene. The ced-3 gene can be used as a
 CC probe or in the prodn. of Ced-3 protein and novel drugs for
 CC enhancing or inhibiting the activity of ICE, ced-3 and related
 CC genes for the treatment of inflammatory diseases and/or diseases
 CC caused by cell death. Novel inhibitors of ced-3 activity include
 CC portions of the ced-3 gene and its product.

SO Sequence 7653 BP; 2429 A; 1456 C; 1270 G; 2498 T; 0 other;

Query Match 2.1%; Score 139.2; DB 17; Length 7653;
 Best Local Similarity 73.3%; Pred. NO. 3.5e-19;
 Matches 211; Conservative 0; Mismatches 63; Indels 14; Gaps 2;

QY 3063 TGTATTGTTACGGGATACAAATTCGAGAAATGCTATTTCACACATATTGACGGC 3122
 DB 1635 TGAATATTATACGGAACACAAATTCAGAAATGCGTATTACAGCATATTGGCGCC 1576
 QY 3123 AAAATATCAGTAGAGAAATCTACGAAATCTTTAAAT-----TTTAAATTTTAC 3176
 DB 1575 AAAATATCTGCTAGCTAGAACTACAGTAATCTTTAAATGACTGACGCTGTGACG 1516
 QY 3177 AATTAAAGAAATACCACTAATCAAAAGAAATTAATTCAAAAATCGCCGTAATC 3236
 DB 1515 ATTATCGGTTATCAAAATTCGAAAAAATATTTCAAAAATTGAGCCGTAATC 1456
 QY 3237 GA-----CTACAGTAGGCAATTTAAGAAATTTAGTATTTGCTACGAGATATTTC 3288
 DB 1455 GACACAAAGCGCTACAGTACATTTAAAGAAATTTAGTATTTGCTACGAGATATTTC 1396
 QY 3289 CGCCTCAATATGTTGTGAATACGATTCACGATTTTGGTCC 3336
 DB 1395 GCGGTCAATATGTTGCGCAGTACCATTTCTAGAAATTTTGATTC 1348

RESULT 4

AAAT72802/c
 ID AAAT72802 standard; DNA: 7653 BP.

AC AAAT72802;

DT 09-FEB-2001 (first entry)

DE ced-3 gene.

XX

KW ced-3; virally induced cell death; apoptosis; gene therapy; neural;
 KW muscular degenerative disease; myocardial infarction; stroke; aging;
 KW interleukin-1beta converting enzyme; ICE; cysteine protease;

KW Ice-ced 3 homologue; Ich; ds.

XX Caenorhabditis elegans.

OS

XX Key Location/Qualifiers

FT misc_signal 2161..2164

FT CDS /*tag= a /label= SL1_splice_acceptor_site

FT exon /*tag= b /product= "Ced-3"

FT intron /*tag= c /number= 1

FT intron 2367..2429 /*tag= d

FT exon /*tag= e /number= 1

FT intron 2430..2575

FT exon /*tag= e /number= 2

FT intron 2576..2853

FT

FT /*tag= f /number= 2
 FT exon 2854..3109 /*tag= g /number= 3
 FT intron 3110..4304 /*tag= h /cons_splice= (5'site:NO,3'site:NO)
 FT exon 4305..4634 /*tag= i /number= 4
 FT intron 4635..5546 /*tag= j /number= 4
 FT exon 5547..5760 /*tag= k /number= 5
 FT intron 5761..5814 /*tag= l /number= 5
 FT exon 5815..5942 /*tag= m /number= 6
 FT intron 5943..6297 /*tag= n /number= 6
 FT exon 6298..6537 /*tag= o /number= 7
 FT intron 6538..7012 /*tag= p /number= 7
 FT exon 7013..7072 /*tag= q /number= 8
 FT intron 7073..7072

PN US6083735-A.

PD 04-JUL-2000.

XX 10-JUN-1994; 94US-0258287.

XX 24-JUN-1993; 93US-0080850.

XX (GEHO) GEN HOSPITAL CORP.

XX Yuan J, Miura M;

XX WPI; 2000-464343/40.

XX P-PSDB; AAB14245.

XX

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XX

Query Match 2.1%; Score 139.2; DB 21; Length 7653;

Example 1; Fig 2; 121pp; English.

The present sequence is the ced-3 gene from *Caenorhabditis elegans*.
 Structural analysis of this gene revealed that it is similar to the
 enzyme interleukin-1beta converting enzyme (ICE) gene and so it is
 thought that Ced-3 acts as a cysteine protease in controlling the onset
 of programmed cell death (apoptosis). The ced-3 gene may be used in gene
 therapy in disorders characterized by cell death e.g. neural and
 muscular degenerative diseases, myocardial infarction, stroke, virally
 induced cell death and aging. The present invention relates to a novel
 human Ice-ced 3 homologue (Ich) gene (AAAT72806), which is homologous to
 the ced-3 gene.

SO Sequence 7653 BP; 2429 A; 1455 C; 1271 G; 2498 T; 0 other;


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FT      /tag= w
FT      /number= Exon_7
FT      Intron 6538..7012
FT      /tag= x
FT      /number= Intron_7
FT      repeat_unit 6567..6625
FT      /tag= y
FT      /rpl_type= INVERTED
FT      /note= "Inverted w.r.t. repeat at 6905-6965"
FT      repeat_unit 6905..6965
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FT      /rpl_type= INVERTED
FT      /note= "Inverted w.r.t. repeat 6567-6625"
FT      exon 7012..7075
FT      /tag= aa
FT      /number= Exon_8
FT      WO9325685-A.
XX      23-DEC-1993.
XX      14-JUN-1993: 93WO-US05701.
XX      12-JUN-1992: 92US-0897788.
XX      20-NOV-1992: 92US-0979638.
XX      (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX      PI Horvitz HR, Shaham S, Yuan J;
XX      WPI: 1994-007542/01.
XX      DR P-PSDB: AAR53281.
XX      PT Isolated C elegans cell death genes ced-3 and ced-4 - used to
XX      PS develop agents to increase or prevent cell death in organisms
XX      Claim 14; Fig 4; 127pp; English.
XX      CC The sequences given in AA064735-45 represent mutations of the C. elegans
XX      CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
XX      CC was most abundant in embryos, but was also detected in larvae and young
XX      CC adults, suggesting that ced-3 is expressed not only in cells undergoing
XX      CC cell death. The four largest introns as well as sequences 5' of the
XX      CC start codon contain repetitive elements, some of which have been
XX      CC characterised in non-coding regions of other C. elegans genes, such
XX      CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
XX      CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
XX      CC region that might be a transmembrane region. One region of ced-3 is
XX      CC very rich in serine. It is thought that this region is involved in
XX      CC protein-protein interactions, similar to acid blobs in transcription
XX      CC factors. Of the mutations which occur within the ced-3 gene, eight of
XX      CC the mutations are missense mutations, these mutations establish the
XX      CC two are putative of the ced-3 gene, confirming that ced-3, like ced-4,
XX      CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
XX      CC function is not essential for viability. The ced-3 and ced-4 gene
XX      CC products may be used to develop agents for treating conditions
XX      CC characterised by cell deaths, such as myocardial infarction, stroke,
XX      CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
XX      CC infection, aging or hair loss.
XX      SQ Sequence 7653 BP; 2430 A; 1453 C; 1271 G; 2499 T; 0 other;
XX
XX      Query Match 2.1%; Score 137.6; DB 15; Length 7653;
XX      Best Local Similarity 72.9%; Pred. No. 7.6e-19;
XX      Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;
XX      3063 TGTATTGTTACGGAATACAAATTCGAGATCTATTTCACACATATTGACGCGC 3122
XX      || ||| ||||| || ||||| || ||||| || ||||| ||||| |||||

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Db      1635 TGAATATTATGAGGAACACAAATTCAGAAATGCGTATTACAGTCATATTGGCGGC 1576
Oy      3123 AAAATATCCAGTAGAAGAACTACAGTAATCTTTAAAT-----TTTAAATTTTAC 3176
Db      1575 AAAATATGCTGCTAGCTGACACACAGTAATCTTTAAATCTACACTGACGTTGTACG 1516
Oy      3177 AATTAAAGAAATTAACACCTAATCAAAAGAAATTAATTTGAAAAATGAGCCGTAATTC 3236
Db      1515 AATTATCGGTTATCAAAATTCGAAAAAAATTAATTTTCAAAAATTTGAGCCGTAATTC 1456
Oy      3227 GA-----CTACAGTAGGCTATTAAAGAAATTCAGTATTGCGCTACGAGATATTTC 3288
Db      1455 GACACAAAGCGCTACAGTAGTCTTAAGAAATTCAGTATTGCGCTACGAGATATTTC 1396
Oy      3289 GCGCTCAATATAGTTGTGAATACGCAATTCAGGATTTTGTGTTCC 3336
Db      1395 GCGCTCAATATAGTTGTGCGCAGTACGCAATTCAGAAATTTTGTGATTC 1348

RESULT 7
AA064738/C
ID      AA064738 standard; DNA: 7653 BP.
XX      AC AA064738;
XX      DT 23-JUN-1994 (first entry)
XX      DE ced-3 (C5940T) gene.
XX      KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
XX      KW embryogenesis; cell death; hydrophilic; transmembrane; region;
XX      KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
XX      KW protein synthesis; null phenotype; calcium-binding domain; ss.
XX      OS Caenorhabditis elegans.
XX
XX      FH Key Location/Qualifiers
XX      FT repeat_unit 1356..1472
XX      FT /tag= a
XX      FT /rpl_type= INVERTED
XX      FT /note= "Inverted w.r.t. repeat at 1490-1614"
XX      FT repeat_unit 1490..1614
XX      FT /tag= b
XX      FT /rpl_type= INVERTED
XX      FT /note= "Inverted w.r.t. repeat at 1356-1472"
XX      FT exon 2232..2366
XX      FT /tag= c
XX      FT /number= Exon_1
XX      FT 2367..2429
XX      FT /tag= d
XX      FT /number= Intron_1
XX      FT 2450..2575
XX      FT /tag= e
XX      FT /number= Exon_2
XX      FT 2576..2853
XX      FT /tag= f
XX      FT /number= Intron_2
XX      FT 2854..3107
XX      FT /tag= g
XX      FT /number= Exon_3
XX      FT 3108..4302
XX      FT /tag= h
XX      FT /number= Intron_3
XX      FT 4326..3243
XX      FT /tag= i
XX      FT /rpl_type= INVERTED
XX      FT /note= "Inverted w.r.t. repeat at 3329-3396"
XX      FT repeat_unit 3329..3396
XX      FT /tag= j
XX      FT /rpl_type= INVERTED
XX      FT /note= "Inverted w.r.t. repeat at 3126-3243"
XX      FT repeat_unit 3487..3759
XX      FT /tag= k

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FT exon
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FT intron
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FT /tag= v
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FT /tag= x
FT /number= Intron_7
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FT /tag= y
FT /rpl_type= INVERTED
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FT repeat_unit
FT /tag= z
FT /rpl_type= INVERTED
FT /note= "Inverted w.r.t. repeat 6567-6625"
FT exon
FT /tag= aa
FT /number= Exon_8

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PT develop agents to increase or prevent cell death in organisms
XX Claim 14; Fig 4; 127pp; English.
PS
XX The sequences given in AA064735-45 represent mutations of the C. elegans
CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
CC was most abundant in embryos, but was also detected in larvae and young
CC adults, suggesting that ced-3 is expressed not only in cells undergoing
CC cell death. The four largest introns as well as sequences 5' of the
CC start codon contain repetitive elements, some of which have been
CC characterised in non-coding regions of other C. elegans genes, such
CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
CC region that might be a transmembrane region. One region of Ced-3 is
CC very rich in serine. It is thought that this region is involved in
CC protein-protein interactions, similar to acid blobs in transcription
CC factors. Of the mutations which occur within the ced-3 gene, eight of
CC the mutations are missense mutations, two are nonsense mutations and
CC two are putative splicing mutations. These mutations establish the
CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
CC function is not essential for viability. The ced-3 and ced-4 gene
CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.
XX
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T; 0 other;
Query Match 2.1%; Score 137.6; DB 15; Length 7653;
Best Local Similarity 72.9%; Pred. No. 7.6e-19;
Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;
QY 3063 TGTATGTTACGGCAATACAAATTCGACAGATCTATTTCACACATATTGAGCGC 3122
DB 1635 TGAATTTATTCAGCAACAAATTCAGCAATTCGATTAATTTGAGCGC 1576
QY 3123 AAAATATTCAGTACGAAATCTACAGTATTTCTTAAAT-----TTTAAATTTTAC 3176
DB 1575 AAAATATTCGATGACGAAATCTACAGTATTTCTTAAATTTGAGCGC 1516
QY 3177 AATTAAAGAAATTAACCAATCAAAAGAAATTAATTCGAAATTCGAGCGC 3236
DB 1515 ATTTACGGGTTATCAAAATTCGAAATTAATTTCTTAAATTTGAGCGC 1456
QY 3237 GA-----CTACAGTACGATTTTAAAGATTTCTGATTTTCTGAGATTTTTC 3288
DB 1455 GACCAAGCGCTACAGTACGATTTTAAAGATTTCTGATTTTCTGAGATTTTTC 1396
QY 3289 CGCCTCAATATGTTGGAATACGATTCAGGATTTTGGTCC 3336
DB 1395 GCGCTCAATATGTTGCGCAGTACGATTTCTGAAATTTTGGATTC 1348

```

RESULT 8
AA064739/c
ID AA064739 standard; DNA; 7653 BP.
XX
AC AA064739;
XX
DT 23-JUN-1994 (first entry)
XX
DE ced-3 (G6297A) gene.
XX
XX C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
OS Caenorhabditis elegans.
XX
XX Key Location/Qualifiers
FH repeat_unit 1356..1472
FT /tag= a

Isolated C elegans cell death genes ced-3 and ced-4 - used to

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FT /rpl_type= INVERTED
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FT repeat_unit
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FT /note= "Inverted w.r.t. repeat at 1356-1472"
FT exon
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FT /number= Exon_1
FT /tag= d
FT /number= Intron_1
FT /tag= e
FT /number= Exon_2
FT /tag= f
FT /number= Intron_2
FT /tag= g
FT /number= Exon_3
FT /tag= h
FT /number= Intron_3
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FT /note= "Inverted w.r.t. repeat at 3329-3396"
FT repeat_unit
FT /tag= j
FT /rpl_type= INVERTED
FT /note= "Inverted w.r.t. repeat at 3126-3243"
FT repeat_unit
FT /tag= k
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FT /note= "Inverted w.r.t. repeat at 3782-4070"
FT repeat_unit
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FT repeat_unit
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FT /number= Exon_4
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FT /rpl_type= INVERTED
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FT repeat_unit
FT /tag= p
FT /rpl_type= INVERTED
FT /note= "Repeat 3"
FT exon
FT /tag= q
FT /number= Exon_5
FT /tag= r
FT /number= Intron_5
FT /tag= s
FT /number= Intron_5
FT /tag= t
FT /number= Exon_6
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FT repeat_region
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FT exon

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FT /number= Intron_7
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FT /rpl_type= INVERTED
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FT repeat_unit
FT /tag= z
FT /rpl_type= INVERTED
FT /note= "Inverted w.r.t. repeat 6567-6625"
FT exon
FT /tag= aa
FT /number= Exon_8
FT W09325685-A.
FT 23-DEC-1993.
FT 14-JUN-1993; 93MO-US05701.
FT 12-JUN-1992; 92US-0897788.
FT 20-NOV-1992; 92US-0979638.
FT (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT Horvitz HR, Shaham S, Yuan J;
FT WPI; 1994-007542/01.
FT Isolated C elegans cell death genes ced-3 and ced-4 - used to
FT develop agents to increase or prevent cell death in organisms
FT
FT Claim 14; Fig 4; 127pp; English.
FT
FT The sequences given in AA064735-45 represent mutations of the C. elegans
FT ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
FT was most abundant in embryos, but was also detected in larvae and young
FT adults, suggesting that ced-3 is expressed not only in cells undergoing
FT cell death. The four largest introns as well as sequences 5' of the
FT start codon contain repetitive elements, some of which have been
FT characterised in non-coding regions of other C. elegans genes, such
FT as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
FT length. Ced-3 is highly hydrophilic with no significant hydrophobic
FT region that might be a transmembrane region. One region of Ced-3 is
FT very rich in serine. It is thought that this region is involved in
FT protein-protein interactions, similar to acid blobs in transcription
FT factors. Of the mutations which occur within the ced-3 gene, eight of
FT the mutations are missense mutations. These mutations establish the
FT two are putative splicing mutations, two are nonsense mutations and
FT null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
FT function is not essential for viability. The ced-3 and ced-4 gene
FT products may be used to develop agents for treating conditions
FT characterised by cell deaths, such as myocardial infarction, stroke,
FT degenerative disease, traumatic brain injury, hypoxia, pathogenic
FT infection, aging or hair loss.
FT
FT Sequence 7653 BP; 2430 A; 1453 C; 1271 G; 2499 T; 0 other;
SQ
Query Match 2.1%; Score 137.6; DB 15; Length 7653;
Best local similarity 72.9%; Pred. No. 7.6e-19;
Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;
QY 3063 TGTATTGTTAGCGGAATGCAAAATTCGCGAATGCTATTTCACAACATATTGACGGCG 3122
DB 1635 TGAATATTATTAGGAGAACCAAAATTCAGAGATGCTATTTCAGCATATTGCGCGCG 1576
QY 3123 AAAATATCCAGTAGAGAAAACAGTAATGCTTTAAAT-----TTTAAATTTTAC 3176
DB 1575 AAAATATGCTAGTAGAAGACTACAGTAATGCTTTAAATGAGTACTAGCGCTGTGACG 1516

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CC was most abundant in embryos, but was also detected in larvae and young
CC adults, suggesting that ced-3 is expressed not only in cells undergoing
CC cell death. The four largest introns as well as sequences 5' of the
CC start codon contain repetitive elements, some of which have been
CC characterised in non-coding regions of other *C. elegans* genes, such
CC as *ced-1*, *lin-12* and *myoD*. The *Ced-3* protein is 503 amino acids in
CC length. *Ced-3* is highly hydrophilic with no significant hydrophobic
CC region that might be a transmembrane region. One region of *Ced-3* is
CC very rich in serine. It is thought that this region is involved in
CC protein-protein interactions, similar to acid blobs in transcription
CC factors. Of the mutations which occur within the *ced-3* gene, eight of
CC the mutations are missense mutations, two are nonsense mutations and
CC two are putative splicing mutations. These mutations establish the
CC null phenotype of the *ced-3* gene, confirming that *ced-3*, like *ced-4*,
CC function is not essential for viability. The *ced-3* and *ced-4* gene
CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.

CC
XX
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T; 0 other;

Query Match 2.1%; Score 137.6; DB 15; Length 7653;
Best Local Similarity 72.9%; Pred. No. 7.6e-19;
Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;

OY 3063 TGTATTGTTACGGAATCAAAATTCGCAATGCTATTTCACACATATTGACGGC 3122
DB 1635 TGAATATTATACGAAACCAAAATTCAGAGATGCGTATTACATATTGCGGCC 1576
OY 3123 AAAATATCCAGTACAGAAATCTACATATCTTTAAAT-----TTTAAATTTTAC 3176
DB 1575 AAAATATGTCGTACGAGAACTACATATCTTTAAATGACTACTGTGCGTTGACG 1516
OY 3177 AATTAAAGAAATATACCACTAATCAAAAGAAATTAATTCAAAATGACCCGTAATTC 3236
DB 1515 ATTTCGCGTTATCAAAATTCGAAAAAATTAATTTCAAAATTTGAGCCGTAATTC 1456
OY 3237 GA-----CTACAGTAGCATTAAAGAAATTTAGTATTTTCCCTGACAGATATTTC 3288
DB 1455 GACACAGACGCTACAGTACATTAAAGAAATTTGCTATTTCCCTGAGATATTTC 1396
OY 3289 CGCCTCAATATGTTGTAATAGCATTCACGATTTTGTGTCC 3336
DB 1395 GCCGTCAATATGTTGCCGACATTCCTCAGAAATTTGTGATTC 1348

RESULT 10
AA064741/c
ID AA064741 standard; DNA: 7653 BP.

XX
AC AA064741;
XX
DT 23-JUN-1994 (first entry)
XX
DE ced-3 (G6372A) gene.
XX
XX C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
XX
OS *Caenorhabditis elegans*.
XX
XX Key Location/Qualifiers
FH repeat_unit 1356..1472
FT /tag= a
FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t. repeat at 1490-1614"
FT 1490..1614
FT /tag= b
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FT /note= "Inverted w.r.t. repeat at 1356-1472"

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FT /tag= d
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FT 2450..2575
FT /tag= e
FT /number= Exon_2
FT 2576..2853
FT /tag= f
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FT 2854..3107
FT /tag= g
FT /number= Exon_3
FT 3108..4302
FT /tag= h
FT /number= Intron_3
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FT /tag= i
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FT /note= "Inverted w.r.t. repeat at 3329-3396"
FT 3329..3396
FT /tag= j
FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t. repeat at 3126-3243"
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FT /tag= k
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FT 3782..4070
FT /tag= l
FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t. repeat 3487-3759"
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FT /number= Exon_4
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FT      23-DEC-1993.
FT      PD
FT      23-DEC-1993.
FT      XX
FT      14-JUN-1993; 93WO-US05701.
FT      XX
FT      12-JUN-1992; 92US-0897788.
FT      PR 20-NOV-1992; 92US-0979638.
FT      XX
FT      (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT      PA
FT      Horvitz HR, Shahan S, Yuan J;
FT      PI
FT      WPI: 1994-007542/01.
FT      DR P-PSDB; AAR53284.
FT      XX
FT      Isolated C elegans cell death genes ced-3 and ced-4 - used to
PT      develop agents to increase or prevent cell death in organisms
PS
PS      Claim 14; Fig 4; 127pp; English.
XX
XX      The sequences given in AAO64735-45 represent mutations of the C. elegans
CC      ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
CC      was most abundant in embryos, but was also detected in larvae and young
CC      adults, suggesting that ced-3 is expressed not only in cells undergoing
CC      cell death. The four largest introns as well as sequences 5' of the
CC      start codon contain repetitive elements, some of which have been
CC      characterised in non-coding regions of other C. elegans genes, such
CC      as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
CC      length. Ced-3 is highly hydrophilic with no significant hydrophobic
CC      region that might be a transmembrane region. One region of Ced-3 is
CC      very rich in serine. It is thought that this region is involved in
CC      protein-protein interactions, similar to acid blobs in transcription
CC      factors. Of the mutations which occur within the ced-3 gene, eight of
CC      the mutations are missense mutations, two are nonsense mutations and
CC      two are putative splicing mutations. These mutations establish the
CC      null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
CC      function is not essential for viability. The ced-3 and ced-4 gene
CC      products may be used to develop agents for treating conditions
CC      characterised by cell deaths, such as myocardial infarction, stroke,
CC      degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC      infection, aging or hair loss.
CC      XX
SQ      Sequence 7653 BP; 2430 A; 1453 C; 1271 G; 2499 T; 0 other:
Query Match 2.1%; Score 137.6; DB 15; Length 7653;
Best Local Similarity 72.9%; Pred. No. 7, 6e-19;
Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;

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QY      3289 GCCTCAAAATATGTGTGAATATACCATTCACCGATTGTTGTGTCC 3336
DB      1395 GCCGTCAAAATATGTGTGGCGAGTACGCATTCTCAGAAATTTGTATTTC 1348
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KW      embryogenesis; cell death; hydrophilic; transmembrane; region;
KW      hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW      protein synthesis; null phenotype; calcium-binding domain; ss.
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FT PD
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FT XX
FT PR 12-JUN-1992; 92US-0897788.
FT PR 20-NOV-1992; 92US-0979638.
FT XX
FT PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT PI Horvitz HR, Shahan S, Yuan J;
FT XX WPI; 1994-007542/01.
FT DR P-PSDB; AAR53286.
FT XX
FT PS Isolated C elegans cell death genes ced-3 and ced-4 - used to
XX develop agents to increase or prevent cell death in organisms
XX Claim 14; Fig 4; 127Pp; English.
XX
XX The sequences given in A0664735-45 represent mutations of the C. elegans
XX ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
XX was most abundant in embryos, but was also detected in larvae and young
XX adults, suggesting that ced-3 is expressed not only in cells undergoing
XX cell death. The four largest introns as well as sequences 5' of the
XX start codon contain repetitive elements, some of which have been
XX characterised in non-coding regions of other C. elegans genes, such
XX as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
XX length. Ced-3 is highly hydrophilic with no significant hydrophobic
XX region that might be a transmembrane region. One region of Ced-3 is
XX very rich in serine. It is thought that this region is involved in
XX protein-protein interactions, similar to acid blobs in transcription
XX factors. Of the mutations which occur within the ced-3 gene, eight of
XX the mutations are missense mutations, two are nonsense mutations and
XX two are putative splicing mutations. These mutations establish the
XX null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
XX function is not essential for viability. The ced-3 and ced-4 gene
XX products may be used to develop agents for treating conditions
XX characterised by cell deaths, such as myocardial infarction, stroke,
XX CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
XX infection, aging or hair loss.
XX
XX SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T; 0 other;
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XX Query Match 2.1%; Score 137.6; DB 15; Length 7653;
XX Best local Similarity 72.9%; Pred. No. 7.6e-19;
XX Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;
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XX || || || || || || || || || || || || || || || || || || ||
XX DB 1635 TGAATATTATAGGAAACCAAAATTCAGAGATCGGATTAAGCATATTGCGCCG 1576
XX || || || || || || || || || || || || || || || || || || ||
XX QY 3123 AAATATTCAGTAGAAGAAATACAGTAATCTTTAAAT-----TTTAAATTTTAC 3176
XX || || || || || || || || || || || || || || || || || || ||
XX DB 1575 AAAATATGTCGATAGCTAGACAGTAATCTTTAAATGACTAGCTAGCTTACG 1516
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XX QY 3237 GA-----CTACAGTAGGCAATTAAGAAATTAAGTAATTTGCGTAGAGATATTTC 3288
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XX DB 1455 GACACAGCGCTACAGTATCAATTAAGAAATTAATTTGCGTAGAGATATTTC 1396
XX || || || || || || || || || || || || || || || || || || ||
XX QY 3289 GGCCTCAATATGTTGGAATACGATTCACGATTTTGTGTTCC 3336
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DB 1395 GCCGTCATATGTCGCCAGTACGCAATTCGAAATTTTGATTC 1348

RESULT 13
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ID AA064744 standard; DNA; 7653 BP.

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AC AA064744;
XX
DT 23-JUN-1994 (first entry)
XX
XX ccd-3 (G6536A) gene.
XX
DE C. elegans; ccd-4; ccd-3; mutant; transcriptional regulation;
XX C. elegans; ccd-4; ccd-3; mutant; transcriptional regulation;
XX embryogenesis; cell death; hydrophilic; transmembrane; region;
XX hydrophobic; mutation; amino acid; substitution; RNA splicing;
XX protein synthesis; null phenotype; calcium-binding domain; ss.
XX
OS Caenorhabditis elegans.

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FH repeat_unit
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XX 12-JUN-1992; 92US-0897788.
XX
XX 20-NOV-1992; 92US-0979638.
XX
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Horvitz HR, Shahan S, Yuan J;
XX
XX WPI; 1994-007542/01.
XX
XX P-PSDB; AAR53287.
XX
XX Isolated C elegans cell death genes ccd-3 and ccd-4 - used to
XX develop agents to increase or prevent cell death in organisms
XX
XX Claim 14; Fig 4; 127pp; English.

The sequences given in AA064735-45 represent mutations of the C. elegans ccd-3 gene. A 2.8 kb mRNA was identified as the ccd-3 transcript and was most abundant in embryos, but was also detected in larvae and young adults, suggesting that ccd-3 is expressed not only in cells undergoing cell death. The four largest introns as well as sequences 5' of the start codon contain repetitive regions of other C. elegans genes, such as characterized in non-coding regions of other C. elegans genes, such as fem-1, lin-12 and myoD. The ccd-3 protein is 503 amino acids in length. Ccd-3 is highly hydrophilic with no significant hydrophobic region that might be a transmembrane region. One region of Ccd-3 is very rich in serine. It is thought that this region is involved in protein-protein interactions, similar to acid blobs in transcription

CC factors. Of the mutations which occur within the *ced-3* gene, eight of
 CC the mutations are missense mutations. Two are nonsense mutations and
 CC two are putative splicing mutations. These mutations establish the
 CC null phenotype of the *ced-3* gene, confirming that *ced-3*, like *ced-4*,
 CC function is not essential for viability. The *ced-3* and *ced-4* gene
 CC products may be used to develop agents for treating conditions
 CC characterised by cell deaths, such as myocardial infarction, stroke,
 CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
 CC infection, aging or hair loss.

XX
 SQ Sequence 7653 BP; 2430 A; 1453 C; 1271 G; 2499 T; 0 other;

Query Match 2.1%; Score 137.6; DB 15; Length 7653;
 Best Local Similarity 72.9%; Pred. No. 7.6e-19;
 Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;

OY 3063 TGTATTTTTCAGGGAATACAAATTCGCAGATGCTATTTCACACATATTTGACGCGC 3122
 DB 1635 TGAATTTTTCAGGGAATACAAATTCGCAGATGCTATTTCACATATTTGCGCGC 1576
 OY 3123 AAAATATCCAGTAGAATACTACGTAATCTTTAAAT-----TTTAAATTTTAC 3176
 DB 1575 AAAAATATCTCGTAGCTACACTACGTAATCTTTAAATGACTGCTGAGCGTTGACG 1516
 OY 3177 AATTAAAGAAATATACCACTAATCAAAAGAAATTAATTCAAAAATGAGCGCGTAATTC 3236
 DB 1515 AATTACGGGTTATCAAAATTCGAAAAAATTAATTTTCAAAATTTGAGCGCGTAATTC 1456
 OY 3237 GA-----CTACAGTAGGATTAATTAAGATTTCTGATGTTTCGCTAGCAGATATTC 3288
 DB 1455 GACACACGCTGACGATGATGATTTAAAGAAATTAATTCGCTAGGTTTCGCTAGCAGATATTC 1396
 OY 3289 CGCCTCAAAATATGTTGTAATACGATTCACGATTTTGTGTTCC 3336
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RESULT 14
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 ID AA064745 standard; DNA; 7653 BP.

XX
 AC AA064745;

DT 23-JUN-1994 (first entry)

DE *ced-3* (C7020T) gene.

XX
 KW *C. elegans*; *ced-4*; *ced-3*; mutant; transcriptional regulation;
 KW embryogenesis; cell death; hydrophilic; transmembrane; region;
 KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
 KW protein synthesis; null phenotype; calcium-binding domain; ss.
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 OS *Caenorhabditis elegans*.

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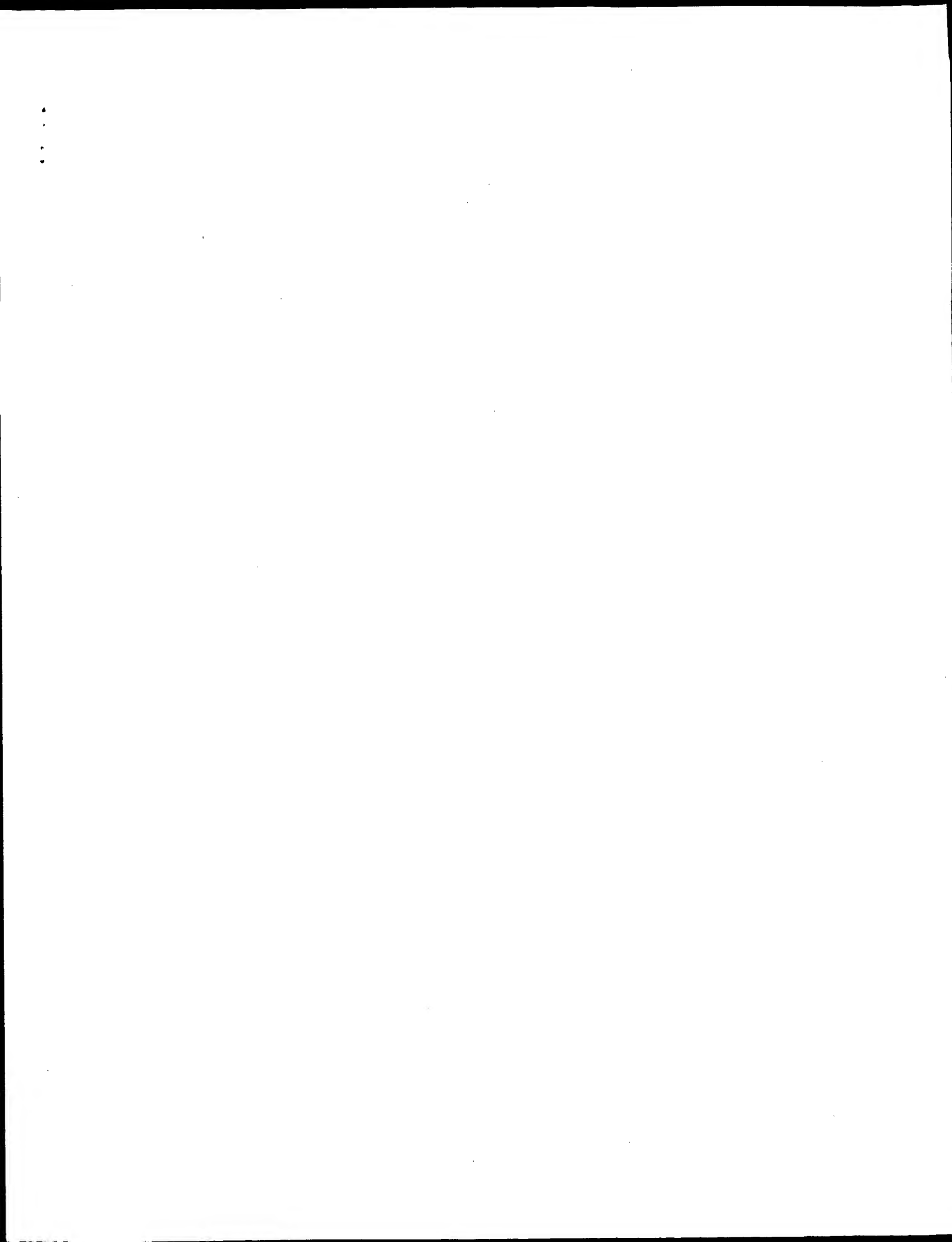
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PD 23-DEC-1993.
XX
PE 14-JUN-1993; 93WO-US05705.
XX
PR 12-JUN-1992; 92US-0897788.
PR 20-NOV-1992; 92US-0984182.
XX
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Horvitz HR, Shaham S, Yuan J;
XX
DR WPI: 1994-007551/01.
DR P-PsDB; AAR45262.
XX
PT Agents which affect activity of cell death genes - used to
PT develop drugs for treating conditions characterised by cell death
PT or proliferation
XX
PS Disclosure: Fig 3; 132pp; English.
XX
CC This sequence encodes the C.elegans cell death gene, ced-3. Fragments
CC of the amino terminal of the protein encoded by this sequence act as
CC inhibitors of ced-3. This gene has considerable similarity to human
CC interleukin-1beta convertase (ICE), which converts pro-interleukin-
CC 1beta to the active cytokine and is involved in inflammatory response
CC in humans. The similarity between the two sequences suggests that
CC inhibitors of ced-3 may also act as inhibitors of ICE. Human ICE and
CC nematode Ced-3 proteins have an overall amino acid similarity of 28%.
CC The ced-3 inhibitors may be used for identifying agents which affect
CC the activity of a gene belonging to the to the ced-3/ICE family of
CC genes and for diagnosis of diseases characterised by cell death. They
CC can also be used to develop drugs for treating conditions characterised
CC by cell deaths such as myocardial infarction, stroke, degenerative
CC disease, traumatic brain injury, hypoxia, pathogenic infection, or
CC hair loss, or drugs for reducing the proliferative capacity or size
CC of a population of cells such as cancerous cells, cells which produce
CC autoreactive antibodies, infected cells, hair follicle cells or cells
CC which are critical to the life of a parasite, pest or recombinant
CC organism. They may also be used in the diagnosis of inflammatory
CC disease.
XX
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T; 0 other;
XX
Query Match 2.1%; Score 137.6; DB 15; Length 7653;
Best Local Similarity 72.9%; Pred. No. 7.6e-19;
Matches 210; Conservative 0; Mismatches 64; Indels 14; Gaps 2;
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DB 1515 ATTTCAGGCTTTCAAAATTCGAAAAAAATTTTTCAAAAATTCAGCCCGGAATTC 1456
OY 3237 GA-----CTACAGTAGCATTAAAGAAATTAAGTATGTTTCGTCAGAGATATTC 3288
DB 1455 GACACAGCGCTACAGTAGTATTTAAAGAAATTAAGTATGTTTCGTCAGAGATATTC 1396
OY 3289 GCGCTCAATATATGTTGTAATATGCAATTCACGGAATTTTGTGTTCC 3336
DB 1395 GACGTCAAATATGTTGCGAGTACGCAATTCGAGAAATTTGATTC 1348

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Search completed: February 27, 2003, 20:35:23
Job time : 1662.38 secs



GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 18:37:30 : Search time 16061.4 seconds

(Without alignments)
11886.551 Million cell updates/sec

Title: US-09-993-420a-1

Perfect score: 6560

Sequence: 1 atcgatagtcgtaccacaaat.....gtttgtataaaatcatcaaa 6560

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 1451402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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30: em_hlg_hum:*
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41: em_hlg_other:*

Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6539.8	99.7	7035	3	CELCTYIA
2	6395.8	97.5	33477	3	CELCTYIA
3	383.2	5.8	3419	3	CELCHHO
4	174.8	2.7	894	3	D78157
5	171.2	2.6	152878	3	CEY18D10A
6	153.4	2.3	42430	3	AF003386
7	149	2.2	34842	3	CEFS4C9
8	145	2.2	43525	3	U88311
9	145	2.2	257728	2	AC006846
10	144.8	2.2	15033	3	CEC56G7
11	143.6	2.2	122720	3	AC025721
12	143.6	2.2	262336	3	AC006786
13	143.4	2.2	56448	3	AC006679
14	142.6	2.2	37794	3	U23139
15	142.6	2.2	309026	2	AC006760
16	142	2.2	36751	2	AC024770
17	140.4	2.1	110000	2	CEY11B2_4
18	140.4	2.1	132742	3	CEY37DBA
19	139.4	2.1	13673	3	AC006672
20	139.4	2.1	299015	2	AC006642
21	139.2	2.1	7653	3	CELCED3A
22	139.2	2.1	7653	6	AR078185
23	139.2	2.1	7653	6	AR102078
24	139.2	2.1	13509	6	AR103124
25	139.2	2.1	13509	6	CEY17G7A
26	139.2	2.1	33477	3	CEY07C4
27	138.6	2.1	26354	3	U61948
28	137.2	2.1	36751	3	AC024770
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30	136.8	2.1	37310	3	CEY18D10A
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33	135.2	2.1	26858	3	CEY36H1
34	135.2	2.1	260699	2	AC024811
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36	135	2.1	306131	2	AC006874
37	135	2.1	23135	3	AC024766
38	135	2.1	122720	3	AC025721
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41	133.2	2.0	40145	3	CEY36A4
42	133.2	2.0	39337	3	U39848
43	132.8	2.0	331326	2	AC006802
44	132.8	2.0	32061	3	AF036693
45	131.8	2.0	58069	3	CEY11B3

ALIGNMENTS

RESULT 1
LOCUS CELCTYIA
DEFINITION Caenorhabditis elegans Cyt-1 (Cyt-1) and CED-9 (ced-9) genes,
complete cds; and unknown gene.
ACCESSION L26545
VERSION L26545
KEYWORDS L26545.1 GI:433174

SOURCE

ORGANISM Caenorhabditis elegans.

Caenorhabditis elegans.

REFERENCE

1 (bases 1 to 7035)
Hengartner,M.O. and Horvitz,H.R.
C. elegans cell survival gene ced-9 encodes a functional homolog of

Pred. No. is the number of results predicted by chance to have a

the mammalian proto-oncogene bcl-2
JOURNAL Cell 76 (4), 665-676 (1994)
MEDLINE 94170367
PUBMED 7907274
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Similarity 100.0%; Pred. No. 0;
Best Local 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
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Qy	301	TTTTSATACAAAAAACTATCCAGACAAACCATVAGACTTTTTCAAATATCTTATTGG	360
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Db	838	CTGTCAATTTGGAAACACCCCATCTTTAAGCTCTCCAGCAAGAGTCTCCACTGGCA	897
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QY	1321	AATGTTGGACAGGTAGAGTGAATTTAATTAATTAATTTAAATTTAAATTAATTT	138
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OY 3301 GTTGTGAATATGCAATTCAGGATTTTGTGTTCCCGGGAATATGCTTAAAGCATTAAT 3360
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Db 3778 GTTGTGAATATGCAATTCAGGATTTTGTGTTCCCGGGAATATGCTTAAAGCATTAAT 3837
OY 3361 TGTGAAATATAAAAATTCAGAAAAAATTCAGAGACATTTCTATGACATCGGAAAAACA 3420
Db 3838 TGTGAAATATAAAAATTCAGAAAAAATTCAGAGACATTTCTATGACATCGGAAAAACA 3897
OY 3421 ATGAAGAGACATTCAGAACGAGAGAAAGCTGAAAAAAGTGGGACCGCGGAAGCAAGAACAG 3480
Db 3898 ATGAAGAGACATTCAGAACGAGAGAAAGCTGAAAAAAGTGGGACCGCGGAAGCAAGAACAG 3957
OY 3481 CGGTGCTGATGATTTGCGCTGGAGTAAACGCTGGAGCCATTTGGAATTCGTTGAGTCTGTC 3540
Db 3958 CGGTGCTGATGATTTGCGCTGGAGTAAACGCTGGAGCCATTTGGAATTCGTTGAGTCTGTC 4017
OY 3541 GTGTGGGCGGATGATTTGAGTTCAGCTTGAAGTAACGATTTCAATTTGTGTAATTAATTAAT 3600
Db 4018 GTGTGGGCGGATGATTTGAGTTCAGCTTGAAGTAACGATTTCAATTTGTGTAATTAATTAAT 4077
OY 3601 TTAATGCAACCTCTTACATTTGAATCTCATTTTGTCTACATGATTTCTCATTCCTTTGA 3660
Db 4078 TTAATGCAACCTCTTACATTTGAATCTCATTTTGTCTACATGATTTCTCATTCCTTTGA 4137
OY 3661 ACTGGAAGATGGGAAAGCTAGGCCAACAAATTCAGGCTCTGTCGATTTACGATTT 3720
Db 4138 ACTGGAAGATGGGAAAGCTAGGCCAACAAATTCAGGCTCTGTCGATTTACGATTT 4197
OY 3721 TACGCAATTTTTCGATTCCTTTTGTGCTTTTGTGGCAAAACCCCTACTCCGGAATATCA 3780
Db 4198 TACGCAATTTTTCGATTCCTTTTGTGCTTTTGTGGCAAAACCCCTACTCCGGAATATCA 4257
OY 3781 ACTTTTCGCTGTTCTGATCATTTTGTCAAAAACCTGAAACCCCTACTTTCTGCGGTG 3840
Db 4258 ACTTTTCGCTGTTCTGATCATTTTGTCAAAAACCTGAAACCCCTACTTTCTGCGGTG 4317
OY 3841 GCTTACCTCCCGCTTCTTCTTCCACATTTCCAAAGTACCCCTGATCTCAATTAATTCATC 3900
Db 4318 GCTTACCTCCCGCTTCTTCTTCCACATTTCCAAAGTACCCCTGATCTCAATTAATTCATC 4377
OY 3901 TTTCACTTAACTGCTCTTCTTCTGCTGGGCTTTCGCAACTCCCGCAAAATTCCTGATCCG 3960
Db 4378 TTTCACTTAACTGCTCTTCTTCTGCTGGGCTTTCGCAACTCCCGCAAAATTCCTGATCCG 4437
OY 3961 GTACGCGACTTTGATTTATTTTTCGAAATTTGTTTCTCTCTCAACAAAAAATTC 4020
Db 4438 GTACGCGACTTTGATTTATTTTTCGAAATTTGTTTCTCTCTCAACAAAAAATTC 4497
OY 4021 GGTCTTTTATTCACACCTTTTTCGAAACGAACCTGCAATTTGATTAATAGGCTGCGC 4080
Db 4498 GGTCTTTTATTCACACCTTTTTCGAAACGAACCTGCAATTTGATTAATAGGCTGCGC 4557
OY 4081 AAGAGAAATCCGTTTTCATTTTTCGCAATCAGTCAATCCAAAAAAGTTATGAGAAATA 4140
Db 4558 AAGAGAAATCCGTTTTCATTTTTCGCAATCAGTCAATCCAAAAAAGTTATGAGAAATA 4617
OY 4141 TCAATTTTAAATTAATGATTCATCTTCTGCGCTTCTGCTGAGAGCAAGGCTCAAT 4200
Db 4618 TCAATTTTAAATTAATGATTCATCTTCTGCGCTTCTGCTGAGAGCAAGGCTCAAT 4677
OY 4201 TCGATGGCTTGAATTTTTCGAAAAAATGTTTTGTTAGTAAAGCATCCCCC 4260
Db 4678 TCGATGGCTTGAATTTTTCGAAAAAATGTTTTGTTAGTAAAGCATCCCCC 4737
OY 4261 GCGTTATTCGCTGTTTACCAATCAGATAGGCTCCGCAATTTGATTCCTGATTTTGTGCG 4320
Db 4738 GCGTTATTCGCTGTTTACCAATCAGATAGGCTCCGCAATTTGATTCCTGATTTTGTGCG 4797
OY 4321 GTATATTAACCAAAAAAGTTAGTACAGATTCAAAAAACAATAGCTGCTTACTAT 4380
Db 4798 GTATATTAACCAAAAAAGTTAGTACAGATTCAAAAAACAATAGCTGCTTACTAT 4857
OY 4381 TCAACTCTGTTTCTTTTGGCTTTTGGCTTTTGTGTTGAGCAAGAGCAATATACAGT 4440
Db 4858 TCAACTCTGTTTCTTTTGGCTTTTGGCTTTTGTGTTGAGCAAGAGCAATATACAGT 4917
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QY 4441 TCAAGGATCAACTATTTGTATAAAGACATTCAGGWRAGTTCCTTGGGAGAA 4500
DB 4918 TCAAGGATCAACTATTTGTATAAAGACATTCAGGWRAGTTCCTTGGGAGAA 4977
QY 4501 AGATTCGTGATTTTCAGTCTTGTATAGCTTGAACGGCTTAAAAAGACATTAAGG 4560
DB 4978 AGATTCGTGATTTTCAGTCTTGTATAGCTTGAACGGCTTAAAAAGACATTAAGG 5037
QY 4561 CCTAAAAATGAACTTTTCCACCGCTTTTCAAAAAAGGCGAATTGACAGCTTTACAC 4620
DB 5038 CCTAAAAATGAACTTTTCCACCGCTTTTCAAAAAAGGCGAATTGACAGCTTTACAC 5097
QY 4621 GAGTTTCTCAATATTTGTATTTGAATTTTCATATTCATCCCAAGCTTTTACAC 4680
DB 5098 GAGTTTCTCAATATTTGTATTTGAATTTTCATATTCATCCCAAGCTTTTACAC 5157
QY 4681 GAAATTTGCAATTTTGGACCTTAAAAATGATACCTGCTGACAGCAAACTTTTGG 4740
DB 5158 GAAATTTGCAATTTTGGACCTTAAAAATGATACCTGCTGACAGCAAACTTTTGG 5217
QY 4741 TTTAAATTCAAAAAGATGCGCCTTTAAAGAGTGTGTGTTGAACCTTCTGTGTGC 4800
DB 5218 TTTAAATTCAAAAAGATGCGCCTTTAAAGAGTGTGTGTTGAACCTTCTGTGTGC 5277
QY 4801 GGAATTTTCATGATTTTTCGTAGCTTTTATTAAGAAAAATGTATTTATTTCAA 4860
DB 5278 GGAATTTTCATGATTTTTCGTAGCTTTTATTAAGAAAAATGTATTTATTTCAA 5337
QY 4861 AAATTTAAATTTAACGAATGCGGAAAAACAAATGAGACACCGATTTAAATTCGAG 4920
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QY 4921 CAACATAGTTGAATTTACATCTCTTTAAAGGNGNCATTTCTATATTTTCACAC 4980
DB 5398 CAACATAGTTGAATTTACATCTCTTTAAAGGNGNCATTTCTATATTTTCACAC 5457
QY 4981 AAATTTGCTGCTCCGNNNGGGGTGCTCATTTTGAAGCAAAATCAGAAAAATTCAT 5040
DB 5458 AAATTTGCTGCTCCGNNNGGGGTGCTCATTTTGAAGCAAAATCAGAAAAATTCAT 5517
QY 5041 ATATGTCGAAAAACACAAATTTATGCGAAATTTCAAGCTTGAAGCAAAATTCAGAAAT 5100
DB 5518 ATATGTCGAAAAACACAAATTTATGCGAAATTTCAAGCTTGAAGCAAAATTCAGAAAT 5577
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DB 5578 TCTAAAAATTTAAAAAAATCATTCGAAATTTGAAATTTGATTTCAACTTGAAGTCAT 5637
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DB 5638 ATGCAAAATTTGCTATTCGCGNNNTTCGANNATTTTGTCCAGGCGCGGCAAAAGAG 5697
QY 5221 AAACGACGANNACTGATTTGCGCAATTTTTCCTGACCGGTCAATTTTGAAGTCAT 5280
DB 5698 AAACGACGANNACTGATTTGCGCAATTTTTCCTGACCGGTCAATTTTGAAGTCAT 5757
QY 5281 TAATAGCTGTATTTTTCGTATTTGACAACTAACTGAATTCATATTTGCAATTTAA 5340
DB 5758 TAATAGCTGTATTTTTCGTATTTGACAACTAACTGAATTCATATTTGCAATTTAA 5817
QY 5341 TATTAAGCTTTGATTTGCTGCTTGAAGAAAAAAACCAAAACCTCATCTAGCTTTAGG 5400
DB 5818 TATTAAGCTTTGATTTGCTGCTTGAAGAAAAAAACCAAAACCTCATCTAGCTTTAGG 5877
QY 5401 TGGCAATATATTTCTAGGACATATAAAACCTTAAATTTCTGCAACCTTACAGC 5460
DB 5878 TGGCAATATATTTCTAGGACATATAAAACCTTAAATTTCTGCAACCTTACAGC 5937
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DB 5938 TATCAAGCTACTATTTAGTATTCATTTTCCAGTCCGACGATGACAAAGCTGCGCTCA 5997
QY 5521 TGCATTCGACAAAGAGAGATTTCTACTTTACCGGATCCGACGAGATCACCTCA 5580
DB 5998 TGCATTCGACAAAGAGAGATTTCTACTTTACCGGATCCGACGAGATCACCTCA 6057
QY 5581 TCTCTCATCTCATATATCACCCACAGTGCACAAAGGAAAGGCGGATGCAACGCTG 5640
DB 6058 TCTCTCATCTCATATATCACCCACAGTGCACAAAGGAAAGGCGGATGCAACGCTG 6117
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QY 5761 GGTTCGTTGTTTGAAG 5820
DB 6238 GGTTCGTTGTTTGAAG 6297
QY 5821 GAAACCGTTGAATTTTAACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5880
DB 6298 GAAACCGTTGAATTTTAACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6357
QY 5881 TTTGCAAGTATTTCTTTGATATTCACAAATTAAGAGAGAGAGAGAGAGAGAGAG 5940
DB 6358 TTTGCAAGTATTTCTTTGATATTCACAAATTAAGAGAGAGAGAGAGAGAGAGAG 6417
QY 5941 GAAACGCAAAATTTAATGGAATGCGGCAACATTTTGAAGAGAGAGAGAGAGAGAG 6000
DB 6418 GAAACGCAAAATTTAATGGAATGCGGCAACATTTTGAAGAGAGAGAGAGAGAGAG 6477
QY 6001 CTACGATATTTCTTCAAAAGACTACTGTAGGCGGTGCGGTTTACAGCTCGATTTT 6060
DB 6478 CTACGATATTTCTTCAAAAGACTACTGTAGGCGGTGCGGTTTACAGCTCGATTTT 6537
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DB 6538 AAATGAATTCACATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6597
QY 6121 AAAAGTCGACCCCTGACTACGATGCTCTTAAAGATTTACTGTATTTTGCATGAG 6180
DB 6598 AAAAGTCGACCCCTGACTACGATGCTCTTAAAGATTTACTGTATTTTGCATGAG 6657
QY 6181 ATATTTGNGGTCAATATGTTGNGCAATAGCAATCTCAGAAATTTGTGTCTGTA 6240
DB 6658 ATATTTGNGGTCAATATGTTGNGCAATAGCAATCTCAGAAATTTGTGTCTGTA 6717
QY 6241 TGTCTGAAATTTTCCATTTCAACATCAATTAAGCAATCTTAAATTTGGGTTCTGCA 6300
DB 6718 TGTCTGAAATTTTCCATTTCAACATCAATTAAGCAATCTTAAATTTGGGTTCTGCA 6777
QY 6301 GCGACGACTATGCTGTATGCGGACAGACGACGACGACGACGACGACGACGACGAC 6360
DB 6778 GCGACGACTATGCTGTATGCGGACAGACGACGACGACGACGACGACGACGACGAC 6837
QY 6361 CAATATCAATTTTAACTATTTAGATTAATTAATTTGGCTAGGAGCTAGGCTGCTT 6420
DB 6838 CAATATCAATTTTAACTATTTAGATTAATTAATTTGGCTAGGAGCTAGGCTGCTT 6897
QY 6421 TTTCACTGCAAAACCTTCAATTTATGCGGCGGCTTCAAAAGAGAGAGAGAGAGAG 6480
DB 6898 TTTCACTGCAAAACCTTCAATTTATGCGGCGGCTTCAAAAGAGAGAGAGAGAGAG 6957
QY 6481 TATTAAGCTTTATATTTATATTTAATTTTGAATTTGATTTGATTTGCAAAAGAGAG 6540
DB 6958 TATTAAGCTTTATATTTATATTTAATTTTGAATTTGATTTGATTTGCAAAAGAGAG 7017
QY 6541 GTTGTATTTAAATTTATC 6558
DB 7018 GTTGTATTTAAATTTATC 7035

Db	10632	CATTTTCCATACCTCTTAACGGAAATCGCTTCTTAGATTCGATTTGGCTAAGGAGATCA	10691
Qy	1320	TAAATGTGGACAGGTAGAGATGTGAAATTTATTAATTTAATGTTTAAATTAATAATTAAT	1379
Db	10692	TAAATGTGGACAGGTAGAGATGTGAAATTTATTAATTTAATGTTTAAATTAATAATTAAT	10751
Qy	1380	TTTCAGATCTACAAATCGGGATATCTGGTATCTGGACTTTGGCTATTTGGCTCGCC	1439
Db	10752	TTTCAGATCTACAAATCGGGATATCTGGTATCTGGACTTTGGCTATTTGGCTCGCC	10811
Qy	1440	ATTGCTCAACTCTTTGGCAGACAAGAGCAACAGACTGCTTAGCAGCATGCTCCG	1499
Db	10812	ATTGCTCAACTCTTTGGCAGACAAGAGCAACAGACTGCTTAGCAGCATGCTCCG	10871
Qy	1500	CTTCTTTTCTTCTTACTCGCCCGCCAGCCTCGACAAATTCGTCAATTTACTTTACCGTT	1559
Db	10872	CTTCTTTTCTTCTTACTCGCCCGCCAGCCTCGACAAATTCGTCAATTTACTTTACCGTT	10931
Qy	1560	GATTTCTTCGATTTTCTCTCTTTCCGTAGATTATACCTCTCTCTCTCTCTCTCTCTCTC	1619
Db	10932	GATTTCTTCGATTTTCTCTCTTTCCGTAGATTATACCTCTCTCTCTCTCTCTCTCTCTC	10991
Qy	1620	TGTCGTGAATGTATATTTATGATTATGAACGAAATTAATTTAGATGACACGCTGCAC	1679
Db	10992	TGTCGTGAATGTATATTTATGATTATGAACGAAATTAATTTAGATGACACGCTGCAC	11051
Qy	1680	GGCGGACAACTCGCTGACGAATCGCGCGATCGGGGAGCAACGATGGCGACTGGCGAGAT	1739
Db	11052	GGCGGACAACTCGCTGACGAATCGCGCGATCGGGGAGCAACGATGGCGAGCTGGCGAGAT	11111
Qy	1740	GAGGAGATTTCTGGGGATTAAGAGCAGAGCCACCGATTTTGAATCATAGTATGTC	1799
Db	11112	GAGGAGATTTCTGGGGATTAAGAGCAGAGCCACCGATTTTGAATCATAGTATGATGC	11171
Qy	1800	TCAGGACTTCGCATCAACCGATTAGCGAGCTTCGACGCGAABAATGTCCATGGGAGATC	1859
Db	11172	TCAGGACTTCGCATCAACCGATTAGCGAGCTTCGACGCGAABAATGTCCATGGGAGATC	11231
Qy	1860	AATTTGATGAAAAATCATATATTGGGAAGCCAAAGGCTTGTATTCGAGCGATTTGTGT	1919
Db	11232	AATTTGATGAAAAATCATATATTGGGAAGCCAAAGGCTTGTATTCGAGCGATTTGTGT	11291
Qy	1920	AATTTTAAATTTTAAATTAATAATTTTCTCTGCTTCGAGCTGCATTTTCC	1979
Db	11292	AATTTTAAATTTTAAATTAATAATTTTCTCTGCTTCGAGCTGCATTTTCC	11351
Qy	1980	GCACCGGAATCCGGGAAACGGAATGGAATGGTTGGAGCACCGGAAATCCCGTGGAGT	2039
Db	11352	GCACCGGAATCCGGGAAACGGAATGGAATGGTTGGAGCACCGGAAATCCCGTGGAGT	11411
Qy	2040	GCAACCGGAGCAGCAAAATGATGCGAGTTATGGAGAGATATTCGAGACAGCAGCGCA	2099
Db	11412	GCAACCGGAGCAGCAAAATGATGCGAGTTATGGAGAGATATTCGAGACAGCAGCGCA	11471
Qy	2100	AAATTTTGAGACCTTCTGTAGGAGCTGCTGCGACGCTCCAGAAATCTCATTTTCACTGTA	2159
Db	11472	AAATTTTGAGACCTTCTGTAGGAGCTGCTGCGACGCTCCAGAAATCTCATTTTCACTGTA	11531
Qy	2160	TCAGATGTGGTGGAGAGGTTGGAAATGCAACACAGATCAATGTCAAATGCTTATGG	2219
Db	11532	TCAGATGTGGTGGAGAGGTTGGAAATGCAACACAGATCAATGTCAAATGCTTATGG	11591
Qy	2220	ACGTTTGGTAAAGGAGAAATACTGAAAAAAAGTTTGCAAAAAATTCGCAAAATTCGCCAGA	2279
Db	11592	ACGTTTGGTAAAGGAGAAATACTGAAAAAAAGTTTGCAAAAAATTCGCAAAATTCGCCAGA	11651
Qy	2280	AAGGTGGGAGAAAAACAATTTGGAAAAATTTGTTTCTTCTTCAGAAAAATTCAGCAAAAC	2339
Db	11652	AAGGTGGGAGAAAAACAATTTGGAAAAATTTGTTTCTTCTTCAGAAAAATTCAGCAAAAC	11711
Qy	2340	TTGGTCAAAAATAGCCAAATATGTGTCTTTTGGAAAGTTTCCATTTAAAAAACACGA	2399

Db	11712	TTGGTCAAAATAATGACCAATTAATGCTCTTTTGTGAAATTTCCATTAATAAAACACAGA	11771
Qy	2400	ATTTCGATCCCGAGATGTGTAATTTTTTTTGTGTGATAAATTAGCAGAAAACCTTAGCAATTC	2459
Db	11772	ATTTCGATCCCGAGATGTGTAATTTTTTTTGTGTGATAAATTAGCAGAAAACCTTAGCAATTC	11831
Qy	2460	GATTBAAAACGTTATTTTCATTCGAAATATTTTAAAGCATATTTTCCCTGATTTGTAT	2519
Db	11832	GATTBAAAACGTTATTTTCATTCGAAATATTTTAAAGCATATTTTCCCTGATTTGTAT	11891
Qy	2520	TGCGAAAAAGATCGTGATTTATCAAAAATCGTTTTTAAATGTBAAAATTTGTGGAAA	2579
Db	11892	TGCGAAAAAGATCGTGATTTATCAAAAATCGTTTTTAAATGTBAAAATTTGTGGAAA	11951
Qy	2580	TACATTTAAATTCGATTTTGTGAACTTTTTTCTCGSAAAAACGTTTTTCTCTGATTTG	2639
Db	11952	TACATTTAAATTCGATTTTGTGAACTTTTTTCTCGSAAAAACGTTTTTCTCTGATTTG	12011
Qy	2640	CTGAACGAAAAACCCCAAAAATTCATTTTCGACATTTAAAAACGAAAAATCGTTTT	2699
Db	12012	CTGAACGAAAAACCCCAAAAATTCATTTTCGACATTTAAAAACGAAAAATCGTTTT	12071
Qy	2700	TTAAGCTTAATTTTCCGCCAGAAATGAAAGCAATTAATTTGCAATTTCTAATTTTCAGAT	2759
Db	12072	TTAAGCTTAATTTTCCGCCAGAAATGAAAGCAATTAATTTGCAATTTCTAATTTTCAGAT	12131
Qy	2760	AGGCTCAATCTGTTGCGCGGTTTCTGATGCGCAAAAATGATGAAATCGTGGAACTGCA	2819
Db	12132	AGGCTCAATCTGTTGCGCGGTTTCTGATGCGCAAAAATGATGAAATCGTGGAACTGCA	12191
Qy	2820	GGGACAAATGCGCAACCTCTTCGTTTACACATCCCTGCTCATCAAAACGGGATCCGCAA	2879
Db	12192	GGGACAAAGTCCGAAACCTCTTCGTTTACACATCCCTGCTCATCAAAACGGGATCCGCAA	12251
Qy	2880	CAACTGGAAGGAACACAAATCGAGCTGGGTAAAGAGATATTTGCATAGACATTAGAACTCA	2939
Db	12252	CAACTGGAAGGAACACAAATCGAGCTGGGTAAAGAGATATTTGCATAGACATTAGAACTCA	12311
Qy	2940	ATAATCCCCCTTCCCTAGTACCCTTGACTTCCGGGGGTGTGTAGAGCCGTAATTTACAG	2999
Db	12312	ATAATCCCCCTTCCCTAGTACCCTTGACTTCCGGGGGTGTGTAGAGCCGTAATTTACAG	12371
Qy	3000	GGTTCGGTACCCTCTTGGGGGGACACTGGGAACATATTCAGATATATTACTGTTTATGA	3059
Db	12372	GGTTCGGTACCCTCTTGGGGGGACACTGGGAACATATTCAGATATATTACTGTTTATGA	12431
Qy	3060	TAAATGTATTGTACGGGAATACAAAATTTGCGAGATGC-TATTTCACAATAATTTTGAC	3118
Db	12432	TAAATGTATTGTACGGGAATACAAAATTTGCGAGATGTGATTTTCACAATAATTTTGAC	12491
Qy	3119	GCGCAAAATATCCAGTATGAGAAATACAGATATTTCTTAATTTTAAAAATTTTTCAA	3178
Db	12492	GCGCAAAATATCCAGTATGAGAAATACAGATATTTCTTAATTTTAAAAATTTTTCAA	12551
Qy	3179	TTAAAGAAAATACCCATTAATCAAAAAGAAATTATTTCAAAAATGAGCCGCTAAATGCA	3238
Db	12552	TTAAAGAAAATACCCATTAATCAAAAAGAAATTATTTCAAAAATGAGCCGCTAAATGCA	12611
Qy	3239	CTACAGTAGGATTTAAAGAAATTAAGTAGTTTTCCTGCTAGCAATATTTTCGCCCTCAAT	3298
Db	12612	CTACAGTAGGATTTAAAGAAATTAAGTAGTTTTCCTGCTAGCAATATTTTCGCCCTCAAT	12671
Qy	3299	ATGTTGTGAATATGCAATTCACGGAATTTTGTGTCTCCCGGGAATATGCTCTTAACCATTA	3358
Db	12672	ATGTTGTGAATATGCAATTCACGGAATTTTGTGTCTCCCGGGAATATGCTCTTAACCATTA	12731
Qy	3359	TTTGTGAAAATPAAAAATCAAGAAAAAATTTGAGAGGCGACTCATGACATCTCGAAAAAC	3418
Db	12732	TTTGTGAAAATPAAAAATCAAGAAAAAATTTGAGAGGCGACTCATGACATCTCGAAAAAC	12791
Qy	3419	AAATGAAAGAGATCTACGAAAGACAGACAGAGCTGAAAAAGTGGAGCCCGGAAGCAGACA	3478
Db	12792	AAATGAAAGAGATCTACGAAAGACAGACAGAGCTGAAAAAGTGGAGCCCGGAAGCAGACA	12851

QY 3479 GACGGTGTGATGATTTGGCGGTGAGTACAGCTGAGCCATTGGATCTGTTGAGATCG 3538
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Db 12852 GAGCGTGTGATGATTTGGCGGTGAGTACAGCTGAGCCATTGGATCTGTTGAGATCG 12911
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QY 3539 TCGTGTGTGGCGGATGATGTTGAGCTTGAAGTACGTTTCAATTTGGTAAATTA 3598
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Db 12912 TCGTGTGTGGCGGATGATGTTGAGCTTGAAGTACGTTTCAATTTGGTAAATTA 12971
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QY 3599 ATTTATGTACACTCTCTTACATTTGATCTCAATTTTGCTCACTGATTTCTCATCTTT 3658
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Db 12872 ATTTATGTACACTCTCTTACATTTGATCTCAATTTTGCTCACTGATTTCTCATCTTT 13031
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QY 3659 GAACGTGAAGTGGGGAAGCTAGGCCCAATTAACGGCTCTGCTGCTGATTTAGAT 3718
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Db 13032 GAACGTGAAGTGGGGAAGCTAGGCCCAATTAACGGCTCTGCTGCTGATTTAGAT 13091
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QY 3719 TTTACGTCAATTTTTCGATTTGCTTTTGGCCAAACCCCTACTCCGCGTAATAT 3778
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Db 13092 TTTACGTCAATTTTTCGATTTGCTTTTGGCCAAACCCCTACTCCGCGTAATAT 13151
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QY 3779 CAACCTTTCGCTGCTGCTGATTTGCTCAAAACCCCTGAACCCCTAATTTTCTGCGCG 3838
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QY 3899 TCTTACATTTACCTGCTCTTCTGCTGCTGCTCTGCACTCCGCCCAATTTCTGTAC 3958
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QY 4317 GTGCGTATATTAACAAAAAGGTAGTGCAGATTCAAAAACCAACAAATGCGTCTTTA 4376
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QY 4377 CTATTCACCTCTGTTCTTTTGGCTTGGCTTGTGAGGCAAGAGAGAGACTATTC 4436
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QY 4616 TACAGAGATTTCTCAATTAATTTGATTTGAATTTTCATATTCATCCCAAGGCTCT 4675
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Db 13991 TACAGAGATTTCTCAATTAATTTGATTTGAATTTTCATATTCATCCCAAGGCTCT 14050
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QY 4676 TACAGAAATTTTGGATTTTGGAGCTTAAATACGATACCTGCTGACACGAAACAT 4735
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QY 4736 TTTTGTAAATTCAAAAAGATGCGCTTTAAAGAGGCTGTTGTTGAACTCTGTT 4795
|||||
Db 14111 TTTTGTAAATTCAAAAAGATGCGCTTTAAAGAGGCTGTTGTTGAACTCTGTT 14170
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QY 4796 GTTGGGACTTTTCATCGATTTTTCGTAGCGTTTAAAGAAATGATTAATTA 4855
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Db 14171 GTTGGGACTTTTCATCGATTTTTCGTAGCGTTTAAAGAAATGATTAATTA 14230
|||||
QY 4856 TTTCAAAATTTTAAATTTTACCGATGCGGAAAAACAAATGAAACACCGATTAATAT 4915
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Db 14231 TTTCAAAATTTTAAATTTTACCGATGCGGAAAAACAAATGAAACACCGATTAATAT 14290
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QY 4916 GCGACCAACATAGTTGAATTAACAGTACTTTTAAAGGNNACATTTCTATATTT 4975
|||||
Db 14291 GCGACCAACATAGTTGAATTAACAGTACTTTTAAAGGNNACATTTCTATATTT 14349
|||||
QY 4976 CACACAACTGTGCTGCTGCGNNNGGTAATGCTATTTGATGCGAAATVCAAGAAAT 5035
|||||
Db 14350 CACACAACTGTGCTGCTGCGNNNGGTAATGCTATTTGATGCGAAATVCAAGAAAT 14409
|||||
QY 5036 TGCATATATGTTCAAAAAACCAATTAATGCGAATTTCAAGCTTGAACGAAATTCAG 5095
|||||
Db 14410 TGCATATATGTTCAAAAAACCAATTAATGCGAATTTCAAGCTTGAACGAAATTCAG 14469
|||||
QY 5096 GAAATTTCAAAATTTAAAAAAATTCATTTGGAATGTAATTTGATTAATCACTGAAG 5155
|||||
Db 14470 GAAATTTCAAAATTTAAAAAAATTCATTTGGAATGTAATTTGATTAATCACTGAAG 14529
|||||
QY 5156 TGCATATGCGAAATTTTC--GTCATATCCGNNNTTCGANNATTTTGTCCAGCGGCGCGCA 5214
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Db 14530 TGCATATGCGAAATTTTC--GTCATATCCGNNNTTCGANNATTTTGTCCAGCGGCGCGCA 14589
|||||
QY 5215 AAAAGAGAGAGAGANNACGATTTTCGCAATTTTTCCTGACGCTGCAATTAATTTG 5274
|||||
Db 14590 AAAAGAGAGAGAGANNACGATTTTCGCAATTTTTCCTGACGCTGCAATTAATTTG 14649
|||||
QY 5275 AAACCTAATTAAGCTGTAATTTTTCGCTATGAGCAACTGATGATTCATTAATTTGCA 5334
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Db 14650 AAACCTAATTAAGCTGTAATTTTTCGCTATGAGCAACTGATGATTCATTAATTTGCA 14709
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QY 5335 TTTAATATTTGACTTTTGTATGTTGCTAGAAAAAAACCAAAAAACCTCATCTAGCT 5394
|||||
Db 14710 TTTAATATTTGACTTTTGTATGTTGCTAGAAAAAAACCAAAAAACCTCATCTAGCT 14769
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QY 5395 TTTAGGCTGCAATTAATTTTCCTGAGACATTAATAAACCTTAATTTCTGCAACACT 5454
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Db 14770 TTTAGGCTGCAATTAATTTTCCTGAGACATTAATAAACCTTAATTTCTGCAACACT 14829
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QY 5455 ACAAGCTATCAACGTAATTAATTAATTTTTCAGAGTCCAGCCGATGACAAAGCTCG 5514
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Db 14830 ACAAGCTATCAACGTAATTAATTAATTTTTCAGAGTCCAGCCGATGACAAAGCTCG 14889
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QY 5515 CTTCAATGCAATTCGAAACAAAGAGAGTTCCTCACTTACCGGATCGAGAGAGATCA 5574
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Db 14890 CTTCAATGCAATTCGAAACAAAGAGAGTTCCTCACTTACCGGATCGAGAGAGATCA 14949
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QY 5575 CTTCAATTCCTCCATACCTCATATACCCCAACTGCAAGTGAAGAGGCGGAGATCA 5634
|||||
Db 14950 CTTCAATTCCTCCATACCTCATATACCCCAACTGCAAGTGAAGAGGCGGAGATCA 15009
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[illegible]

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              /gene="ced-9"
Intron        /number=3
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              /number=3
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              /number=4

BASE COUNT   976 a      727 c      668 g      1035 t      13 others
ORIGIN

Query Match   5.8%; Score 383.2; DB 3; Length 3419;
Best Local Similarity 61.9%; Pred. No.2:5e-61;
Matches 860; Conservative 0; Mismatches 385; Indels 147; Gaps 10;

QY  963 TTACAGTCCGAGGCAAGACCCCAATCCAGAGTTCCGATGGGAAATACCTGTTGAAGCA 1022
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    775 TTTTCAGTGGAGGCAAAAGCTCTATTCAAAAGTTCCGATGGGAAATACCTCAGAGCA 834

QY  1023 GCGCTCCAGAAATCGCCCAATCGTCACATCTCACCGCTTACACGCCAATTGACCTG 1082
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    835 GCGGCACATGAAGACCGCCATGCTCACATCTCACCGCTTACACGCCAATTGACCTG 894

QY  1083 GATGCTCTCGGATTCATAGAAATCAGCGGTTGTATATGCGCGAACCCTTCCTGCTGG 1142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    895 GATGCTCTCGGATTCATAGAAATCAGCGGTTGTATATGCGCGAACCCTTCCTGCTGG 954

QY  1143 AGGAATCGGATTCGAGTTTGGCTTGCATTCACCGCTTTTGGATTCATCCGCTAG 1202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    955 TGGACTCGGATTCGCGCTTTCATCTGATTTTCCACCGCTTTCGATGATACATCCGCTGG 1014

QY  1203 CTGGAATCTTACCATCGCGGTGACCGCTGTCTTCA----- 1237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1015 ATGGAATCTTACCATCGCTGTGTTACCGCTGTCTTCAAGGTAATCGTTTATTTATA 1074

QY  1238 -----AGTACATCATTTGCTTCCCATTCATTTTCCATAC 1271
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1075 GTTGTATTTTGAATTTCTAATTTTATGATCATCATCGCATTCGCATTCATCTCCATAC 1134

QY  1272 TCTTAACGGAATTCGCTCTTAAGATCGAATTTGGCTAAGAGAGTCATATATTTGGACA 1331
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1135 TCTTAACGGAATTCGCTCTTAAGATCGAATTTGGCTAAGAGAGTCATATATTTGGACA 1194

QY  1332 GGTAGAGCTTAAATTTATTTATTTTAAATTTAAATTTAAATTTATTTATTTGATCTAC 1391
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1195 GGT-----ATTTTCAAGTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCA 1243

QY  1392 AAATCGGATATCTGATCTGAGCTTGGCTATTTCTGCTCGCATTTGCTTCAAC 1451
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1244 AAATCGGATATCTGATCTGAGCTTGGCTATTTCTGCTCGCATTTGCTTCAAC 1303

QY  1452 TCTTCCAGCAAGACAGACAA-----CAAGCTGCTAGGCAACAGATTCCTCCGCTTCTT 1505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1304 TCTTCCAGCAAGACAGACAA-----CAAGCTGCTAGGCAACAGATTCCTCCGCTTCTT 1363

QY  1506 TTTTCTTATCTCGCCCGCCGCTGACAAATTTCTCAATTTACTTTTACCGCTGATTTT 1564
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1364 TTTTCTTATCTCGCCCGCCGCTGACAAATTTCTCAATTTACTTTTACCGCTGATTTTCTTA 1423

QY  1565 -----CTTGATTTTCTCTTCTTTCCG 1586
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    1424 GGTGTTATTAATTCACCTGCGCCCTTGTACCAACCCGTTCCGCTGATCCGCCCATCCG 1483

QY  1587 TAGATTACCTCTCTCTCTGTTTCTTCTCTGCTGATAGT-----ATATTAGA 1640
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1484 TCAGATTATACCGCTGCTCTTTTCTCTGATAGATTTATCGTTTCTTCCAAATGAT 1543

QY  1641 TTTTGAAGAGATTAATTTTAA-----GATGACACGCTGACGCGGCAACATCTGCT-- 1694
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1544 ATTTTAAACAAATTAATTTTATGATGATGACACGCGGATGCAATGATGATTCGATGAG 1603

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QY  1695 -----GACGAATCCGCGGTATGCGGAGCAACGATGCGCACTGCGCATGTA 1741
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1604 ATATGCAAACTGCTGCGCAATATCTTCCGAGGAGGCAATGCGCACAAATGAAATGA 1663

QY  1742 AGGAGTTTCTGGGGATTAAGGCAAGACCGCCACCGATTTTGAATCAATAGTGATGTC 1801
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    1664 GAGAGTTTCTTATCAACAAAAGACGAGCGCACACACTTGGGAATGACATATACCA 1723

QY  1802 AGGAGTTTSCATACCGCATAGGACGCTTTCGACCGGAAGAAATTCATTCGAGAGTCAA 1861
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1724 A-----ATCACCGACTCTTACGACACCAATGAAAGAGATGCAATTTGAGATTCAA 1774

QY  1862 TTGATGAAAAATCATGATGATGGAAGAGCCGCTGATATATGAGGATTTTGCTGTA 1921
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    1775 -----CCAGAAATTTATGATTTGGAAGAACCTCGGTTTAAACATTCAGGATTTGTTAA 1828

QY  1922 TTTTATATTTTATTTTGTAAATTAATTTCTGCTGCTTCCAGGTGATTTTCAACGC 1981
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1829 GCATTTATTTTGAAGATGCTGTAGTGTGAATGTTTATTAAGTTGATGATTTTCAAT 1888

QY  1982 ACCGAATCCGGCAAAACGGAATGGAATGTTTGGACACCGGATTTGCCGTGGAGTGC 2041
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    1889 ATCGCATACGACAAAATGCTCTAGATTTGTATGATGCGCTGATTTACCGATGAGATTG 1948

QY  2042 AACCGAGCAGCAAAATGATGCGAGTTTATGGAAGAGATTTGGAAGAGACAGCGGAAA 2101
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1949 AAAAGAGCATGAGATGATGATGCGATCATTTGGGACGATTTTGAAGAAAACACATGAGA 2008

QY  2102 ATTTGAGACCTTCTGTGATGACGATGCTGCGATGCGCCAGATCTCATTTTCACTGATC 2161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    2009 TCTTGAAGAACTCTCTTAAACACTACTTGCATTTCCAAAATTAAGTTTCAATTCAGC 2068

QY  2162 AGAATGTGTTTCGAGCGGTTGGAATGACAGACAGATGATCAATGCAATGCTTATGAGAC 2221
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    2069 AAGAAGTGTGAGACGCTGTTGGAATTTCAATCAACACACCGCTTCCATGATCTTACGAGC 2128

QY  2222 GTTTGTAG 2231
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    2129 GTTTGTAG 2138

```

```

RESULT 4
D78157
LOCUS
DEFINITION D78157 894 bp mRNA linear INV 08-APR-2000
complete cds.
ACCESSION D78157
VERSION D78157.1 GI:1817529
KEYWORDS cytochrome b-large subunit.
SOURCE Ascaris suum mitochondrial cDNA to mRNA.
ORGANISM Ascaris suum Mitochondrion; Nematoda; Chromadorea; Ascarididae;
1 (sites)
REFERENCE 1 (sites)
AUTHORS Kita,K., Hirawake,H. and Takamiya,S.
TITLE Cytochromes in the respiratory chain of helminth mitochondria
JOURNAL International Journal for Parasitology (1997) In press
REFERENCE 2 (bases 1 to 894)
AUTHORS Kita,K.
TITLE cDNA cloning of cytochrome b large subunit of mitochondrial
fumarate reductase from Ascaris suum
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 894)
AUTHORS Kita,K.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-1995) Kiyoshi Kita, The Institute of Medical
Science, The University of Tokyo, Parasitology; 4-6-1 Shirokanedai,
Minato-Ku Tokyo 108, Japan (E-mail:kitak@ims.u-tokyo.ac.jp,
Tel:03-5449-3570, Fax:03-5449-5410)
FEATURES
source
1..894
/organism="Ascaris suum"
/organelle="mitochondrion"

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COMMENT

On May 14, 2001 this sequence version replaced gi:3900862. Coding sequences below are predicted from computer analysis, using predictions from GeneFINDER (P. Green, U. Washington), and other available information. Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is not the entire insert of clone Y18D10A. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions. The true left end of clone F08A8 is at 152766 in this sequence. The true right end of clone B0019 is at 105 in this sequence. The start of this sequence (1..105) overlaps with the end of sequence AL008866. The end of this sequence (152766..152878) overlaps with the start of sequence Z99710. For a graphical representation of this sequence and its analysis see: <http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=Y18D10A> IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

FEATURES

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/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"

/chromosome="1"
/clone="Y18D10A"

join(AL008866.1:35941..36134,AL008866.1:38497..38616,AL008866.1:38680..38844,AL008866.1:39643..39790,106..164,1247..1523,3116..3199,3300..3397,3451..3672,3805..3991)

/gene="B0019.3"
join(AL008866.1:35941..36134,AL008866.1:38497..38616,AL008866.1:38680..38844,AL008866.1:39643..39790,106..164,1247..1523,3116..3199,3300..3397,3451..3672,3805..3991)

/gene="B0019.3"
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DYVNNRQIPQQTSSRSRLKNSAKEDVPHSDHFKKANDSDSMEDADLSNYSKYR
NDLPSPSPISSTSRKSRKRPKSAPEAHVAPTEKLELLEPNEPEIKOETIDEDON
VPVLEKPEKISVYPPRISPTESINVEKWEETQESERLRREMDDEEIDEDON
DIIDPRLDNAFODIEESIROFNCRKNSVDLDNDHACFDVRSQAHFSDSAS
LIGNSNIGVPDEDSIDPTKITYAFWTGLVHEGHFLOGGDNLPKILVSDVNP
MLFGKNRIVLSVILMDPEARDVKNKLTGPGEYSVHHISKNIPFVPPYSWLSHLAA
IVLATDRICGRPLSNLELEKLAADPEIEMASSKYEVSIKAKMKRGLRAMRALD
EAVNNRPL"

complement(join(7920..8081,9752..9924,10879..11164,12369..12659,13906..14204,15129..16655,17748..18104,19860..19949,20008..20088,20709..20807,22205..23127,24486..24744,25724..25909,26020..26130,26236..26256))

/gene="Y18D10A.1"
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/gene="Y18D10A.1"
/note="predicted using GeneFINDER
cDNA EST YK541b5.5 comes from this gene"

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/protein_id="CAA22308.1"

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/db_xref="SPTREMBL:O9XW25"

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/db_xref="taxon:6253"
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32..598
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/codon_start=1
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/db_xref="GI:1817530"

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YLMQRAIKRPIAPHLITVYKPMWVMSVGLHRTGCAAGATLIGVGVSVPDIDPTT
FVEPRGIGMPWVILDTDFKFIAPFHLNGLIRFIDPMAGTIDIPSYSGAVLV
GLAALISLAVVVSVERHKATLPTNH"

BASE COUNT 191 a 214 c 215 g 274 t
ORIGIN

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Best Local Similarity 68.4%; Pred. No. 2.2e-22;

Matches 242; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

970 TCCGAGGCAAAACGCCATCCAGAAAGTTGGATGGAATACCTGTGAGCAGCGCTCC 1029

125 TCGGGGAGAAACACCGATTCAGGTGGGCTGGATATCTGATGAGGAGCGTGG 184

1030 AAGAAATCGCCCATCGCTCCACATCTCAACCGTCTACCAAGCCAAATGACCTGATGCTC 1089

185 CTCMAAGCAGCCATCGCCCCCATCTTACCATCTACAAAGCCAGATGATGATGCTG 244

1090 TCCGATTCCTCAGATCAGCGGTTGTAAATGCGCGCAACCTCTCGTGGAGGAATC 1149

245 TCCGGCTCCACCGAGTTCACGATGCGCTGAGGCTGGACCTTGTGATTTGGTGGGTC 304

1150 GGATTCGAGTTTGGCGTTCGATTCACCGCTTTTGTGATTCATCCGATGCTGGAAC 1209

305 GCGTTTCGCTGTTCGATTCATGACCTGACGAGCTTGTGAATTCATGAGAGATGGGC 364

1210 TTACATGCGCGGTGACCGCTGCTTCAAGTATCATTCATCTTCCCATCTTTCAT 1269

365 ATACCATGGGTGATCTCTGATCTTCAATTTATTTATGCGCTCCGATTCGATTCAC 424

1270 ACCTTAAGCAATTCGCTTAGATTCGATTCGATTCGATTCGATTCGATTCGATTC 1323

425 ACCTCATGGAATTCGCTTTCATCGATTCGATTCGATTCGATTCGATTCGATTC 478

RESULT 5
CEY18D10A 152878 bp DNA linear INV 24-JUN-2002
LOCUS
DEFINITION
Caenorhabditis elegans cosmid Y18D10A, complete sequence.
ACCESSION
AL034393.1 GI:3979928
VERSION
AL034393.1 GI:3979928
KEYWORDS
HTG.
SOURCE
Caenorhabditis elegans.
ORGANISM
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE
1 none.
AUTHORS
TITLE
Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
JOURNAL
Science 282 (5396), 2012-2018 (1998)
MEDLINE
98059613
PUBMED
9851916

REMARK
2 (bases 1 to 152878)
REFERENCE
AUTHORS
TITLE
Direct Submission
JOURNAL
Submitted (17-DEC-1998) Nematode Sequencing Project, Sanger
Institute, Hinxton, Cambridge CB10 1SA, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or tw@nematoe.wustl.edu

CDS

gene

CDS

VERSION AF003386.1 GI:2088833
 KEYWORDS HTG.
 SOURCE Caenorhabditis elegans.
 ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabdilitida; Rhabdilitidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 42430)
 AUTHORS Waterston, R.
 TITLE Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium
 JOURNAL Science 282 (5396), 2012-2018 (1998)
 MEDLINE 99069613
 PUBMED 9851916
 REFERENCE 2 (bases 1 to 42430)
 AUTHORS Johnson, D.
 TITLE The sequence of C. elegans cosmid F59E12
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 42430)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAY-1997)
 REFERENCE 4 (bases 1 to 42430)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
 REFERENCE 5 (bases 1 to 42430)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (21-SEP-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
 REFERENCE 6 (bases 1 to 42430)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (05-MAY-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
 REFERENCE 7 (bases 1 to 42430)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (22-MAY-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
 COMMENT Submitted by:
 Genome Sequencing Center
 Department of Genetics, Washington University
 St. Louis, MO 63110, USA, and
 Sanger Centre, Hinxton Hall
 Cambridge CB10 1RQ, England
 email: twenematode.wustl.edu and jessesanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m33 subclone.

For a graphical representation of this cosmid sequence and its analysis see:
<http://www.wormbase.org/db/seq/sequence?name=F59E12;class=Sequence>

NEIGHBORING COSMID INFORMATION

The 5' cosmid is C17G10, 5100 bp overlap; the 3' cosmid is C25H3, 200 bp overlap. Actual start of this cosmid is at base position

FEATURES

source
 misc_feature
 gene
 CDS

2488 of F59E12; actual end is at 3056 of C25H3.

NOTES:
 Coding sequences below are the result of integration and manual review of the following data: computer analysis using the program GeneFinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yujin Kohara (http://www.ddo.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORPOME cloning project (http://wormdb.dcl.harvard.edu/), similarity to other proteins from Blast analysis (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research, 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

Location/Qualifiers

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 /db_xref="taxon:6239"
 /chromosome="11"
 /clone="F59E12"
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 /note="SL1 transcription acceptor; see yk52894.5"
 5464..7284
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 /note="For a graphical representation of this gene see: <http://www.wormbase.org/db/seq/sequence?name=F59E12.5a;class=Sequence>"
 join(5464..5607,5659..6024,6087..6278,6326..7058,7130..7284)
 /gene="F59E12.5"
 /note="contains similarity to Pfam domain PF00641 (zf-RanBP), Score=20.2, E-value=0.015, N=1; coded for by the following C. elegans cDNAs: yk53d12.5, yk661h5.3, yk661h5.5, yk723d3.3"
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    yk603c12.5, yk68h8.3, yk121c6.3, yk69a2.3, yk288b8.3,
    yk279e7.3, yk539e6.3, yk603c12.3, yk68h8.5, yk121c6.5,
    yk279e7.5, yk288b8.5, yk539e6.5, yk208a12.5"
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    OKEMASPTIDHOQVCELTFTTISMLETAIDMADVHNENHSEEROLYINQ
    TKSNREKEFKSPQPKPVKNQVSNOSQKPKPKPTOPANSSCYKLTGLIVH
    VGSSEKGEHYSEVLONESSRMSKFDSDRVSNRMEDVAOSGTSSTASACILIV
    AKMDGYDDMSDMVIRNDPSTPAVISEEVIDPDLDPNFGTGGCKPDVYNE
    NDTISLSDPREOFREKMRNSECVNHIAIPGCGYVLADPRISDYRCITTAOL
    VLAMRIADMKPFYHDIKMMNLITLPTTRRLVETNIDKTTITTFGILLIDFSK
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Query Match      2.3%; Score 153.4; DB 3; Length 42430;
Best Local Similarity 61.1%; Pred. No. 1.4e-18;
Matches 276; Conservative 0; Mismatches 173; Indels 3; Gaps 2;

CDS
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    17755 ATTTTCTCGAATTTATGCTGTGATGAAGACGATTATCCAGACGCAAAATTTGAGATA 17814
    4695 TTGAGCTTAATACGATACCTGCTCGACACGAAACATTTTGTAAATTCAAAAG 4754
    17815 TTGCGCTAAATAATACATACCTGCTCGCGCGCAAGTTTGTGAAATGCCGTAG 17874
    4755 ATGAGCGCTTTAAAGAGCTGTACTTTGAACCTTCTGTTCCGACCTTTTCATGA 4814
    17875 GTGTGCGCTTTGAGAGAGCGGTATTTCAATTTTAATTCGACGAATTTTCATCGA 17934
    4815 TTTTGTGACGCTTTTATAGAAATGTAT--TTATTATTCAAAATTTTATTTT 4872
    17935 TTTTTCATAGTTATTTGATGAAACATATTTTATTAATTAATAAACTTTAATAGCTATA 17994
    4873 ACCGATCGGGAACAAATGAGACACCGATTAATAAATATTCGACCAACAATAGTTT 4932

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Db 17995 GGAGCATATTAATTTTAACTCGAGAAAATATAGAAAGTTCGCAAAAACGAAATTC 18054
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Db 18055 CAATATACAGTACTCTTTTAAGGNGCCAGCCACTT--TTCCATTTTAAATAATTTGTCATG 18113
Qy 4993 TCGNNCNGCGTATGCTCATTTTGAATGCAAGAAATTCAGAAATTTGATTTGCAAAA 5052
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Qy 5053 AACCAATATTAGCGCAATTTTCAGCTTTGAAA 5084
Db 18174 AACACGATAGTATGAAACAAACGATGTAACAAA 18205

RESULT 7
LOCUS      CEF54C9
DEFINITION Caenorhabditis elegans cosmid F54C9, complete sequence.
ACCESSION  Z49967
VERSION    249967.1
KEYWORDS   HTG; 60S ribosomal protein L5; Collagen; GTP-binding
           ADP-ribosylation factor; Heat shock 70Kd; HSP70; Initiation factor
           5A; Pim110.
SOURCE     Caenorhabditis elegans.
ORGANISM   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
           Caenorhabditis elegans.
REFERENCE  1 Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
           2 (bases 1 to 34842)
           Sims, M.A.
           Direct Submission
           Submitted (30-JUN-1995) Nematode Sequencing Project, Sanger
           Institute, Hinxton, Cambridge CB10 1SA, England and Department of
           Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
           jess@anger.ac.uk or rwm@nematode.wustl.edu
           Coding sequences below are predicted from computer analysis, using
           predictions from GeneFinder (P. Green, U. Washington), and other
           available information.
           Current sequence finishing criteria for the C. elegans genome
           sequencing consortium are that all bases are either sequenced
           unambiguously on both strands, or on a single strand with both a
           dye primer and dye terminator reaction, from distinct subclones.
           Exceptions are indicated by an explicit note.
           This sequence is the entire insert of clone F54C9. The true right
           end of clone W0109 is at 11134 in this sequence. The start of this
           sequence (1..101) overlaps with the end of sequence Z49969.
           The end of this sequence (34733..34842) overlaps with the start of
           sequence Z68315.
           for a graphical representation of this sequence and its analysis
           see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
           name=F54C9
           IMPORTANT: This sequence is NOT necessarily the entire insert of
           the specified clone. It may be shorter because we only sequence
           overlapping sections once, or longer because we arrange for a small
           overlap between neighbouring submissions.
           location/Qualifiers
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           /chromosome="II"
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FEATURES
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    gene
    CDS

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yk746.5 comes from this gene
CDNA EST yk83d2.5 comes from this gene; CDNA EST yk82f11.5
comes from this gene
CDNA EST yk117a6.5 comes from this gene; CDNA EST
yk11a5.5 comes from this gene; CDNA EST yk96h9.5
comes from this gene
CDNA EST yk115c3.5 comes from this gene; CDNA EST yk83b7.3
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CDNA EST yk58g11.5 comes from this gene; CDNA EST
yk85b10.5 comes from this gene
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yk11a5.3 comes from this gene
CDNA EST yk82f11.3 comes from this gene; CDNA EST
yk461f1.3 comes from this gene
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yk674g4.3 comes from this gene
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yk523h3.5 comes from this gene
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yk530a5.5 comes from this gene
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yk533e4.5 comes from this gene
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yk605f8.5 comes from this gene
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complement(join(9858. .10050,10484. .10573,10657. .11023,
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CDNA EST yk261c3.3 comes from this gene
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gene
CDS

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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 257728)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (24-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

FEATURES

source
1 237702: contig of 237702 bp in length
* 237703 237715: gap of unknown length
* 237716 247715: contig of 10000 bp in length
* 247716 247728: gap of unknown length
* 247729 257728: contig of 10000 bp in length.
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/db_xref="taxon:6239"
/clone="Y119C17"

BASE COUNT 82806 a 46012 c 45799 g 83085 t 26 others
ORIGIN

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Best Local Similarity 62.3%; Pred. No. 4.4e-17;

Matches 308; Conservative 0; Mismatches 172; Indels 14; Gaps 5;

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DB 38667 ATGAAGCGAAAGCAAAATTCGCTAATAAAGCAATATACCCAGAGCT--AAATTT 38610
QY 4697 TGAGCTTAAATACGATACCGTCTGACACGAAACATTTTGTAAATTCAAAAGAT 4756
DB 38609 TTGCGCAAAATACGATACCGGCTCGACAGATTTAGTTAGTCGCAAAA--AT 38551
QY 4757 GTGCGCTTTAAAGAGTCTGAGTTGAACCTCTGTGCGGACTTTTATGATTT 4816
DB 38550 GTGCGCTTTAAAGAGTCTGATTAATTAACCTTTGTGCTGCGGAAATTTATCGATT 38491
QY 4817 TTTCGACCTTTTATTAAGAAAATGATTTATTTATTCAAAATTTATTTACCG 4876
DB 38490 TCTTTTAAAGTGTCTCAATTAACATGT--TTTAACATTTAAAAATTTGATTTTCCA 38432
QY 4877 AATCGCGAAAATGAAGAAACACCGATTAATATGCGACGAACATAGTTTGAAA 4936
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QY 4997 NNCGGTATCGTCATTTTATGAGAAATCAAGAAATTTGATATATGTTAAAAAAC 5056
DB 38320 GACGCTTACCGT--ATTTTATGCAAAAATCGCAGATTTGAAATATAGATTAATTCAC 38262
QY 5057 ACAATTATGCGGAA 5070
DB 38261 AAACCTTTGTGAA 38248

RESULT 10
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LOCUS CEC5667
DEFINITION Caenorhabditis elegans cosmid C5667, complete sequence.

ACCESSION 246793
VERSION 246793.1
KEYWORDS HMG; Lys-tRNA; Myosin regulatory light chain 2; transfer RNA.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE

AUTHORS

TITLE

JOURNAL none.
MEDLINE Investigating biology. The C. elegans Sequencing Consortium
PUBMED Science 282 (5396), 2012-2018 (1998)
99069613
9851916

REMARK

The C.elegans Sequencing Consortium.
2 (bases 1 to 15023)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (25-NOV-1994) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jess@sanger.ac.uk or rwnematode.wustl.edu
Coding sequences below are predicted from computer analysis, using predictions from GeneFinder (P. Green, U. Washington), and other available information.
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
For a graphical representation of this sequence and its analysis see: <http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=C5667>
IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
IMPORTANT: This sequence is not the entire insert of clone C5667. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
The true left end of clone C5667 is at 22095 in sequence Z34800.
The true left end of clone F5992 is at 14924 in this sequence. The start of this sequence (1..305) overlaps with the end of sequence Z34800.
The end of this sequence (14929..15023) overlaps with the start of sequence Z34801.

FEATURES

source

gene

CDS

Join(complement(4854..5045),complement(4564..4765),complement(3435..3517),complement(2786..2928),complement(2661..2743),complement(2408..2602),complement(1885..2186),complement(1333..1648),complement(640..888),complement(122..440),complement(234800..1:39244..39590),complement(234800..1:38425..38537),complement(234800..1:38267..38378))
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DEFINITION Caenorhabditis elegans cosmid Y48G8AL, complete sequence.
 AC025721
 VERSION AC025721.2 GI:13559692
 KEYWORDS HTG.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida;
 Rhabdilitoidae; Rhabdilitidae; Pelodierinae; Caenorhabditis.
 REFERENCE
 AUTHORS 1 (bases 1 to 122720)
 TITLE Waterston, R.
 JOURNAL Genome sequence of the nematode C. elegans: a platform for
 MEDLINE investigating biology. The C. elegans Sequencing Consortium
 PUBMED 99069613
 REFERENCE 9851916
 AUTHORS 2 (bases 1 to 122720)
 TITLE Murray, J. and Du, H.
 JOURNAL The sequence of C. elegans cosmid Y48G8AL
 REFERENCE Unpublished (2001)
 AUTHORS 3 (bases 1 to 122720)
 TITLE Waterston, R. H.
 JOURNAL Direct Submission
 REFERENCE Submitted (12-MAR-2000) Genome Sequencing Center, Washington
 TITLE University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 REFERENCE MO 63108, USA
 AUTHORS 4 (bases 1 to 122720)
 TITLE Waterston, R.
 JOURNAL Direct Submission
 REFERENCE Submitted (06-APR-2001) Department of Genetics, Washington
 TITLE University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE 5 (bases 1 to 122720)
 TITLE Waterston, R.
 JOURNAL Direct Submission
 REFERENCE Submitted (07-SEP-2001) Department of Genetics, Washington
 TITLE University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
 REFERENCE MO 63110, USA
 AUTHORS 6 (bases 1 to 122720)
 TITLE Waterston, R.
 JOURNAL Direct Submission
 REFERENCE Submitted (16-NOV-2001) Department of Genetics, Washington
 TITLE University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
 REFERENCE MO 63110, USA
 AUTHORS 7 (bases 1 to 122720)
 TITLE Waterston, R.
 JOURNAL Direct Submission
 REFERENCE Submitted (19-APR-2002) Department of Genetics, Washington
 TITLE University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
 REFERENCE MO 63110, USA
 COMMENT On Apr 6, 2001 this sequence version replaced gi:7230345.
 Submitted by:
 Genome Sequencing Center
 Department of Genetics, Washington University
 St. Louis, MO 63110, USA, and
 Sanger Centre, Hinxton Hall
 Cambridge CB10 1RO, England
 email: twenematode.wustl.edu and jesusanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
 It may be shorter because we only sequence overlapping sections
 once, or longer because we provide a small overlap between
 neighboring submissions.

This sequence was finished as follows unless otherwise noted: all
 regions were double stranded, sequenced with an alternate chemistry
 or covered by high quality data (i.e., phred quality >= 30); an
 attempt was made to resolve all sequencing problems, such as
 compressions and repeats; all regions were covered by sequence from
 more than one m13 subclone.

For a graphical representation of this cosmid sequence and its
 analysis see:
www.wormbase.org/db/seq/sequence?name=Y48G8AL;class=Sequence

NEIGHBORING COSMID INFORMATION

The 5' cosmid is 2K993, 200 bp overlap; the 3' cosmid is Y48G8AR,
 200 bp overlap.

NOTES:

Coding sequences below are the result of integration and manual
 review of the following data: computer analysis using the program
 GeneIndex (P. Green and L. Hillier, personal communication), the
 large scale EST projects of Yujl Kohara
 (http://www.ddb.jig.ac.jp/c-elegans/blm/CE_INDEX.html) and The C.
 elegans ORFome cloning project (<http://worldb.dfci.harvard.edu/>),
 similarity to other proteins from Blastx analyses
 (<http://blast.wustl.edu/>), sequence conservation with C. briggsae
 using Jim Kent's WABA alignment program (Genome Research
 10:115-1125, 2000), individual C. elegans Genbank submissions,
 and personal communications with C. elegans researchers. TRNAS
 are predicted using the program tRNAscan-SE (Lowe, T.M. and
 Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

FEATURES

source

1. 122720

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/strain="Bristol N2"

/db_xref="taxon:6239"

/chromosome="I"

/clone="Y48G8AL"

/complement(4007..8513)

/note="for a graphical representation of this gene see:
www.wormbase.org/db/seq/sequence?name=Y48G8AL.9;class=Sequence"

CDS

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/protein_id="AAK29910.1"

/db_xref="GI:13559704"

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 RLVQSDSDSEMDNLFSTIAHNTKTSVSSFTRECEIDIDPTKRASDAHFYSDHPT
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/complement(13194..21875)

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/note="for a graphical representation of this gene see:
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/codon_start=1

/product="Hypothetical protein Y48G8AL.10"

/protein_id="AAK29901.2"

/db_xref="GI:20198899"

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 TDPRGRTICFSCDKTHAPSRFSATIGVAVHLSDDLECCGNEFENEDLDH
 IRRHSTVDLEVFCEPKCKVLTLESASHLSAONSVKIRRSASAPPEKPPK
 ASHTGKGVREKRTVGNAKOIVCRIGSFSKRIYFSEILNFORSHDRMLKAI
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 CKREFRPAKMLEKRRRPHLLAEHRWRLILHGGGSGEKCTCDMSFLVLSLVNM
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gene
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    /note="for a graphical representation of this gene see:
    [www.wormbase.org/db/seq/sequence?name=Y48G8AL.14;class=Se
    quence]"
    CDS
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        CESSAC08R, YK117d7.3, YK117d7.5, YK117e6.3, YK17e6.5,
        YK18f9.3, YK412b10.3, YK412b10.5, YK79g12.5, YK648c5.5,
        YK648h5.3, YK648h5.5, YK74d41.3, YK84b07.3, YK81b08.3,
        YK89a08.3, YK809f03.3, YK809f03.5, YK801d08.3,
        YK801d08.5, YK89a08.5, YK833b02.3, YK761a04.5,
        YK801d08.3, YK833c07.3, YK811b08.5, YK79b03.5, CEMS92,
        YK805f09.3, YK833c07.3, YK822g11.3, YK85a03.5,
        YK1004f12.3, CEESG28, CESSAC08, YK822g11.3, YK85a03.5,
        YK822g11.5, YK124d02.5, YK1053a09.5, YK1057c05.5,
        YK1136a07.5, YK1182f01.5, YK122a11.5, YK122h02.5,
        YK1284d01.5, YK1285c09.5, YK1296d10.5, YK1306c12.5,
        YK114e07.5, YK1053a09.3, YK1057c05.3, YK1117b04.3,
        YK1136a07.3, YK1156b09.3, YK1182f01.3, YK1213b11.3,
        YK122a11.3, YK1240e04.3, YK1244b02.3, YK1261b03.3,
        YK1284d01.3, YK1285c09.3, YK1296d10.3, YK1300b04.3,
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Best Local Similarity 79.5%; Pred. No. 8e-17;
Matches 221; Conservative 0; Mismatches 49; Indels 8; Gaps 4;

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OY 3299 ATGTGTGAATACGCAATTCAGGATTTTGTGTCCC 3336
Db 44683 ATGTGTGAATACGCAATTCAGGATTTTGTGTCCC 44646

RESULT 12
AC006786/c
LOCUS
DEFINITION
    Caenorhabditis elegans clone Y48G8, *** SEQUENCING IN PROGRESS ***
ACCESSION
    AC006786.2
VERSION
    HTG: HTGS_PHASE1.
KEYWORDS
    Caenorhabditis elegans.
SOURCE
    Caenorhabditis elegans
ORGANISM
    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
    Rhabditidae; Rhabditidae; Pelodierinae; Caenorhabditis.
REFERENCE
    1 (bases 1 to 262336)
    Waterston, R.H.
    The sequence of Caenorhabditis elegans clone
    2 (bases 1 to 262336)
    Waterston, R.H.
    Direct Submission
    Submitted (23-FEB-1999) Genome Sequencing Center, Washington
    University School of Medicine, 444 Forest Park Parkway, St. Louis,
    MO 63108, USA
COMMENT
    On Mar 1, 1999 this sequence version replaced gi:4263152.
    * NOTE: This is a 'working draft' sequence. It currently
    * consists of 13 contigs. The true order of the pieces
    * is not known and their order in this sequence record is
    * arbitrary. Gaps between the contigs are represented as
    * runs of N, but the exact sizes of the gaps are unknown.
    * This record will be updated with the finished sequence
    * as soon as it is available and the accession number will
    * be preserved.
    1
    13925: contig of 13925 bp in length
    13926 13934: gap of unknown length
    13935 16026: contig of 2092 bp in length
    16027 16035: gap of unknown length
    16036 81454: contig of 65419 bp in length
    81455 81463: gap of unknown length
    81464 161281: contig of 79818 bp in length
    161282 161290: gap of unknown length
    161291 163945: contig of 2655 bp in length
    163946 163954: gap of unknown length
    163955 167128: contig of 3174 bp in length
    167129 167137: gap of unknown length
    167138 202845: contig of 35708 bp in length
    202846 202854: gap of unknown length
    202855 205084: contig of 2230 bp in length
    205085 205093: gap of unknown length
    205094 209517: contig of 4424 bp in length
    209518 209526: gap of unknown length
    209527 221793: contig of 12267 bp in length
    221802 221802: gap of unknown length
    221803 228079: contig of 6277 bp in length
    228080 228088: gap of unknown length
    228089 231641: contig of 3553 bp in length
    231642 231649: gap of unknown length
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        /db_xref="taxon:6239"

BASE COUNT      83490 a 46255 c 46078 g 84102 t 2411 others
ORIGIN
Query Match      2.2%; Score 143.6; DB 2; Length 262336;
Best Local Similarity 79.5%; Pred. No. 8e-17;
Matches 221; Conservative 0; Mismatches 49; Indels 8; Gaps 4;

```


REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Louis, MO 63110, USA
8 (bases 1 to 56448)
Waterston, R.
Direct Submission
Submitted (21-DEC-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St Louis, MO 63110, USA
9 (bases 1 to 56448)
Waterston, R.
Direct Submission
Submitted (19-APR-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St Louis, MO 63110, USA
On Mar 1, 2000 this sequence version replaced gi:4263259.
Submitted by:

Genome Sequencing Center
Department of Genetics, Washington University
St. Louis , MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
email: tw@emacode.wustl.edu and jess@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

For a graphical representation of this cosmid sequence and its analysis see:
[\[www.wormbase.org/db/seq/sequence?name=R13A5;class=Sequence\]](http://www.wormbase.org/db/seq/sequence?name=R13A5;class=Sequence)

NEIGHBORING COSMID INFORMATION

The 5' cosmid is C07H6, 200 bp overlap; the 3' cosmid is Y80D4G, 2683 bp overlap.

NOTES:

Coding sequences below are the result of integration and manual review of the following data : computer analysis using the program GeneFinder (P. Green and U. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C elegans ORFome cloning project (<http://worfdb.dcdi.harvard.edu/>), similarity to other proteins from Blastx analyses (<http://blast.wustl.edu/>), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. TRNAs are predicted using the program tRNAscanner-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

Location/Qualifiers

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/clone="R13A5"
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/gene="ceh-13"

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codon_start=1
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/translation="MSSNEQYGGAPPHNYODMPYTHSYSPVSESSYPLNHHPADIMA AHSNT IAGNGHVSPPATASGLSPASSSSSALDELGYASQHNHTYKMMTKRSOR PAAPKRVVIDENGTRINFTTHQILEKEPHYKAYNRRRPFIAISNLKLGSAQYKI WFONRMRKEKKEKKAFLARNTWESNPSVSSCGEDVKNKF"
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protein_id="AAK84464.1"
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complement(29124..31387)
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/note="for a graphical representation of this gene see:

Query Match 2.2%; Score 143.4; DB 3; Length 56448;
Best Local Similarity 66.6%; Pred. No. 1e-16;
Matches 233; Conservative 0; Mismatches 108; Indels 9; Gaps 2;

CDS

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36924 ACACGAAATTTTGCATTTTGCATTTTAAATFAGCAATACCTGCTGACGACGAAATAT 36983
4737 TTTGTAATTTTGCATTTTGCATTTTAAATFAGCAATACCTGCTGACGACGAAATAT 4796
36984 TTTGTAATTTTGCATTTTGCATTTTAAATFAGCAATACCTGCTGACGACGAAATAT 37043
4797 TTGCGACTTTTGCATTTTGCATTTTAAATFAGCAATACCTGCTGACGACGAAATAT 4856
37044 ATGTGGAAATTTTATGATTTT--TAATGATTAAGTAAATGATTTTAAATTTT 37101
4857 TCAAAATTTTATTTTACGATTCGGAATAAATGAAATGATTTTAAATTTTAT 4916
37102 TCA-----CTTTTAACTAATAATTAATTTTAAATTTTAAATTTTAAATTTT 37154
4917 GCAGCAATATTTTGAATTAATTAATTAATTAATTAATTAATTAATTTTAAATTTT 4976
37155 GCAGCAATATTTTGAATTAATTAATTAATTAATTAATTAATTTTAAATTTTAA 37214
4977 ACACAAATTTTGCATTTTGCATTTTAAATFAGCAATACCTGCTGACGACGAAAT 5026
37215 CAACAACTTTGCTGTCGACGACGACGACGACGACGACGACGACGACGACGACGAAAT 37264

RESULT 14
023139
LOCUS 023139 37794 bp DNA linear INV 22-MAY-2002
DEFINITION Caenorhabditis elegans cosmid F13H8, complete sequence.
ACCESSION 023139
VERSION 023139.1 GI:722370
KEYWORDS HMG.
SOURCE
ORGANISM
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae;
Rhabditidae; Rhabditidae; Pelodidae; Caenorhabditis.
1 (bases 1 to 37794)
Waterson, R.
Genome sequencing of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)
JOURNAL MEDLINE 99069613
PUBMED 9851916
REFERENCE
AUTHORS 2 (bases 1 to 37794)
TITLE Ding H.
JOURNAL The sequence of C. elegans cosmid F13H8
REFERENCE 3 (bases 1 to 37794)
AUTHORS Waterson, R.
TITLE Direct Submission
JOURNAL Submitted (13-JUL-1995)
REFERENCE 4 (bases 1 to 37794)
AUTHORS Waterson, R.
TITLE Direct Submission
JOURNAL Submitted (11-APR-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 37794)
AUTHORS Waterson, R.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
REFERENCE 6 (bases 1 to 37794)

AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA

COMMENT

Submitted by: Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
email: twenematecode.wustl.edu and jess@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m33 subclone.

For a graphical representation of this cosmid sequence and its analysis see:
<http://www.wormbase.org/db/seq/sequence?name=F13H8;class=Sequence>

NEIGHBORING COSMID INFORMATION

The 5' cosmid is T24H7, 300 bp overlap; the 3' cosmid is C29F5, 200 bp overlap. Actual start of this cosmid is at base position 297 of F13H8; actual end is at 37794 of F13H8.

NOTES:

Coding sequences below are the result of integration and manual review of the following data: computer analysis using the program GeneFinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddb.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFome cloning project (<http://wormfdb.dcel.harvard.edu/>), (http://blast.wustl.edu/) sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans GenBank submissions, are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucleic Acids. Res., 25, 955-964).

FEATURES

source

1.37794
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/strain="Bristol N2"
/db_xref="taxon:6239"
/chromosome="I"
/clone="F13H8"
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<http://www.wormbase.org/db/seq/sequence?name=F13H8.5;class=Sequence>"

gene

CDS

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gene

CDS

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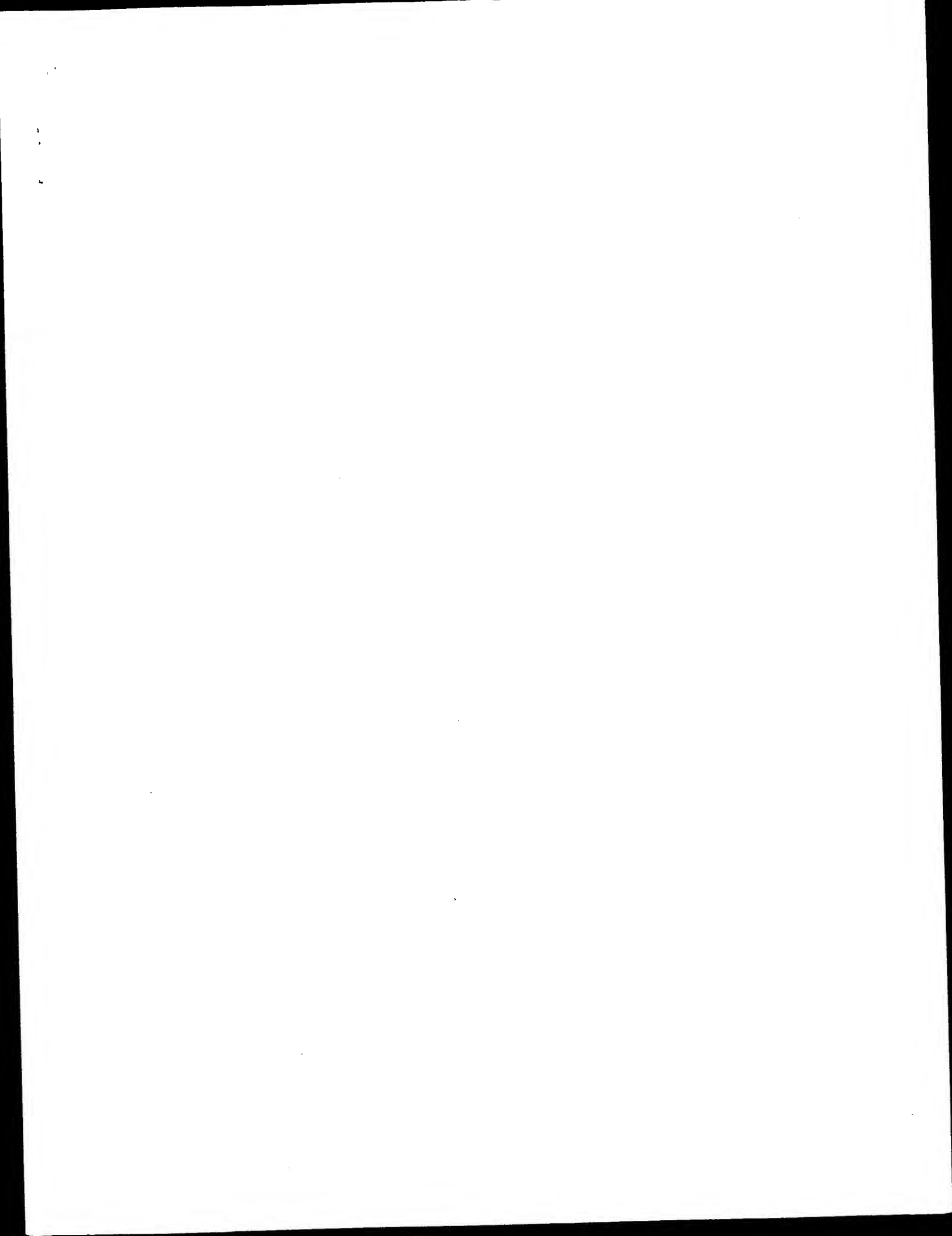
gene

CDS

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gene

CDS



	Query Match	99.7%;	Score 6541.8;	DB 5;	Length 6560;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 6560; Conservative	0;	Mismatches	0;	Gaps
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OY	61 CAAATCTCGACAATAAGAAGATGCAAGSATTATGAAGAGGTGCCGAATCTAAATATTT	120			
Dd	61 CAAATCTCGAAAAGAAGAGATCAGAAGATTAAGAAGAGTGTCGAATCTAAATATTT	120			
OY	121 TAATTAAAAAAATCAATTCGAATTGAAATTCAACTCCTACTCGTTTTGAAATAGCCA	180			
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Dd	181 TCCTTAGTAGTAACCTTCGSAATCGGCCCATTTCTTCCACAATAATTCCTTCAAAGTAGTGT	240			
OY	241 TTGACTAGTATTCCTCGCAAGAATAGAACCTTTCGAATCTCCGSGAGCGCAAGCGGAT	300			
Dd	241 TTGACTAGTATTCCTCGCAAGAATAGAACCTTTCGAATCTCCGSGAGCGCAAGCGGAT	300			
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Dd	301 TTTSATATACAAAAACATATCCAGACAAACCATAGACATTTTCAAAATATTTCTTATTTGG	360			
OY	361 CTGTGCATTTGGAGACACCCCAATCTTTAAAGCCTTCGACGCGAGAAGTCTTCACATCGCCA	420			
Dd	361 CTGTGCATTTGGAGACACCCCAATCTTTAAAGCCTTCGACGCGAGAAGTCTTCACATCGCCA	420			

Oy	4 21	AGGATAAAAGCTCATTTTGTAGAGCCGAATTTTACTAAAATCTGACGATGGATGCAT	480
Db	4 21	AGGATAAAAGGCTCATTTTTGTAGAGCGAATTTTACTAAAATCTGACGATGGATGCAT	480
Oy	4 81	GGATAGAAATTCGAGGAATTTTACATTTTCATCTTGAAATTTTGCATGAAAAATAATT	540
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Db	6 61	ACTTCTGTGCCCTGTGCGTGCAATTTCCGCAACAAATTCACACTGTTTGGAAACGA	720
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Db	11 41	GGAGGAATTCGGAATTCGCGAGTTTTCGCCGTGTGATTCACGCGTTTTGTGATTCATCCGT	1200
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Oy	14 41	TTGTCTTAACCTTCGCGAGAAACAAGACAACAACTGCTAGGACAGATGCTCGGCG	1500
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RESULT 2
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; Sequence 1, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Hengartner, H. Robert
; APPLICANT: Horvitz, H. Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; EARLIER FILING DATE: 1999-01-20
; EARLIER FILING DATE: 1992-06-12
; EARLIER FILING DATE: 1992-06-12
; EARLIER FILING DATE: 1992-06-12
; EARLIER FILING DATE: 1992-08-10
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; EARLIER FILING DATE: 1994-08-10
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

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: LENGTH: 6559
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(6559)
: OTHER INFORMATION: n = A,T,C or G
US-09-234-186-1

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Query Match      99.5%; Score 6529.8; DB 4; Length 6559;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6559; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 1621 GTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1681 GCGGACACCTGCTGACGATTCGCGCTGATGCGGACGACGATGCGGACGATG 1740
DB 1681 GCGGACACCTGCTGACGATTCGCGCTGATGCGGACGACGATGCGGACGATG 1740
QY 1741 AAGGATTTCTGCGGATTAAGGCAAGAGCCGCTGCTGCTGCTGCTGCTGCTGCT 1800
DB 1741 AAGGATTTCTGCGGATTAAGGCAAGAGCCGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 1801 CAGGATCTCCATCAGCGAGTAGGAGGCTTGCAGCGCAAAATGTCATGAGAGTCA 1860
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QY 1861 ATTGATGAGAAATCAATGATGAGGCAAGAGCTTGAATGAGAGGATTTGAGTGA 1920
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QY 1921 ATTTTAAATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 1980
DB 1921 ATTTTAAATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 1980
QY 1981 CACGGAATCCGCAAAACGGAATGATGCTTTGAGACACCGGATTCGCTGAGAGTG 2040

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QY 4201 TCGATGGCCTGATATTTTCGAAAAAATGTTTGTAGCTAAAGATCCCCC 4260
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QY 4261 GCGTATCGCTGTTTCACCATCAGATAGGCTCCGCCATTTGATCCCTGGAATTTGCG 4320
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QY 4321 GTATATTAACAAAAAGCTAGTGCACGATTCAAAAACACATGCGTCTTACTAT 4380
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Db 5820 GAAACCGTTGAATTTTAACCTTGACAGTAAGAAAATTGGCGATTAATGTCACAT 5879
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Db 5880 TTTGCCAGTATATCTTTGTGATATCAATTAACGAAGTCAAAAGCAGAAATATTCG 5939
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Db 5940 GAAACCAAAATTAATGAGATGCGACACATATTTGACCGCAAAATATCTCGTAGCGAA 5999
Oy 6001 CTACAGTATTTCTCAAAAGACTAGTACGCTGCTGTCGATTTTCGAGCTGATTTTTCG 6060
Db 6000 CTACAGTATTTCTCAAAAGACTAGTACGCTGCTGTCGATTTTCGAGCTGATTTTTCG 6059
Oy 6061 AAATGATCAGACTAGAGAAAAGAGAGCAAAATATTTGAACATCATTTGAACATCAATCA 6120
Db 6060 AAATGATCAGACTAGAGAAAAGAGAGCAAAATATTTGAACATCATTTGAACATCAATCA 6119
Oy 6121 AAAAGTCGACCTTGACTACAGTACTGCTTCTAAAGAAATTAAGTATTTTCGTCAGAG 6180
Db 6120 AAAAGTCGACCTTGACTACAGTACTGCTTCTAAAGAAATTAAGTATTTTCGTCAGAG 6179
Oy 6181 ATATTTTNGNGTCAATATGTTGNGCAATGCGATCTCGAATTTGCTGTCGTA 6240
Db 6180 ATATTTTNGNGTCAATATGTTGNGCAATGCGATCTCGAATTTGCTGTCGTA 6239
Oy 6241 TCTCTGAAAATTTTTCATTTCAACATCAATTAAGCAATCAATTAAGTGGTTCGTA 6300
Db 6240 TCTCTGAAAATTTTTCATTTCAACATCAATTAAGCAATCAATTAAGTGGTTCGTA 6299
Oy 6301 GCGACCATATGACGTGATGCTGGCAAGACCCACTCGAAAACCTAGCTGTCCTTTAA 6360
Db 6300 GCGACCATATGACGTGATGCTGGCAAGACCCACTCGAAAACCTAGCTGTCCTTTAA 6359
Oy 6361 CAATATCAATTTTAAATTTAGTATTAATAAATTTGGCTAGCAGCTGCGGCTT 6420
Db 6360 CAATATCAATTTTAAATTTAGTATTAATAAATTTGGCTAGCAGCTGCGGCTT 6419
Oy 6421 TTTGAGTGAACAACTTTAATTTAATCGCGGCTCTTCAAAAAGTGGTTCCTTTGAAA 6480
Db 6420 TTTGAGTGAACAACTTTAATTTAATCGCGGCTCTTCAAAAAGTGGTTCCTTTGAAA 6479
Oy 6481 TATAAGCTTATATATTTATATTAATAAATTTGATTAATGATATCAAAAGCGACTA 6540
Db 6480 TATAAGCTTATATATTTATATTAATAAATTTGATTAATGATATCAAAAGCGACTA 6539
Oy 6541 GTTTGTATATAAATTTATCA 6560
Db 6540 GTTTGTATATAAATTTATCA 6559

RESULT 4
US-09-234-186-2
; Sequence 2, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; EARLIER FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/899,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
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;; EARLIER APPLICATION NUMBER: 08/288,295
;; EARLIER FILING DATE: 1994-08-10
;; EARLIER APPLICATION NUMBER: 08/801,248
;; EARLIER FILING DATE: 1997-02-19
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: PasteSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 1315
;; TYPE: DNA
;; ORGANISM: Caenorhabditis elegans
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (77)...(846)
US-09-234-186-2

Query Match          9.6%; Score 632.6; DB 4; Length 1315;
Best Local Similarity 99.8%; Pred. No. 5.9e-138;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3393 GGACGACTTCATGACACTCGGAAAACAATGAAAGAGACTAGAACGACAGACACTGA 3452
Db 669 GGACGACTTCATGACACTCGGAAAACAATGAAAGAGACTAGAACGACAGACACTGA 728
Oy 3453 AAAAGTGGAGCGCGGGAAGAGAGACAGCGGTGATGATTTGGCGTGGAGTAACAGC 3512
Db 729 AAAAGTGGAGCGCGGGAAGAGAGACAGCGGTGATGATTTGGCGTGGAGTAACAGC 788
Oy 3513 TGGAGCCATTGGAATCGTTGAGTCTGCTGCTGGAGCGATGATGTCAGCTTGAAGTA 3572
Db 789 TGGAGCCATTGGAATCGTTGAGTCTGCTGCTGGAGCGATGATGTCAGCTTGAAGTA 848
Oy 3573 ACGATATCAATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3632
Db 849 ACGATATCAATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
Oy 3633 TTTGCTCAGTATTTCTCTATCTTCCTTGAAGTGAAGAGGGAAGGGAAGGCAACAAT 3692
Db 909 TTTGCTCAGTATTTCTCTATCTTCCTTGAAGTGAAGAGGGAAGGGAAGGCAACAAT 968
Oy 3693 TACGGCTCTGTGTCGATTTAGATTTAGTCAATTTTTCGATTCCTTTTTCCTTTT 3752
Db 969 TACGGCTCTGTGTCGATTTAGATTTAGTCAATTTTTCGATTCCTTTTTCCTTTT 1028
Oy 3753 GGGCAAAACCTTCTCGGGTAAATCAACTTTTCGCTGTCGATTTGTCAAAAA 3812
Db 1029 GGGCAAAACCTTCTCGGGTAAATCAACTTTTCGCTGTCGATTTGTCAAAAA 1088
Oy 3813 CCCTGAACCCTAACCTTTCTCGCGGCTAGACCTCCGCTTCCTTCACATTTTCCA 3872
Db 1089 CCCTGAACCCTAACCTTTCTCGCGGCTAGACCTCCGCTTCCTTCACATTTTCCA 1148
Oy 3873 AAGTACCCCTGATTCATTAATTCATCTTCACTTAACTGTCCTTTTCGTCGTCCTC 3932
Db 1149 AAGTACCCCTGATTCATTAATTCATCTTCACTTAACTGTCCTTTTCGTCGTCCTC 1208
Oy 3933 TTTCAACTCCGCCCAAAATCTGTACGCGTAGCGCACTTGTATTAATTTTCAATTT 3992
Db 1209 TTTCAACTCCGCCCAAAATCTGTACGCGTAGCGCACTTGTATTAATTTTCAATTT 1268
Oy 3993 GTTTTCCTCTCAACACACAAAAAAGCGTTC 4025
Db 1269 GTTTTCCTCTCAACACACAAAAAAGCGTTC 1301

RESULT 5
US-09-234-186-4
; Sequence 4, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
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; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
; US-09-234-186-4

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Query Match          9.6%; Score 632.6; DB 4; Length 1315;
Best Local Similarity 99.8%; Pred. No. 5.9e-138;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 3393 GGAGGACTTCATGACACTCGGAAAAACAATGANAAGAGACTACGACAGCAGAGCTGA 3452
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Db 669 GGAGGACTTCATGACACTCGGAAAAACAATGANAAGAGACTACGACAGCAGAGCTGA 728
QY 3453 AAAAGTGGAGCGCGGAAAGCAGACAGAGCGGTGATGATGCGCTGGAGTAACAGC 3512
    |||
Db 729 AAAAGTGGAGCGCGGAAAGCAGACAGAGCGGTGATGATGCGCTGGAGTAACAGC 788
QY 3513 TGGAGCCATTGGAATCGTTGGAGTCTGCTGTGGGCGGATGATGTTCACTTGAAGTA 3572
    |||
Db 789 TGGAGCCATTGGAATCGTTGGAGTCTGCTGTGGGCGGATGATGTTCACTTGAAGTA 848
QY 3573 ACGTATTCATTTGTGTAATAATTAATTTATGTAACAACCTCTTACATTTGAATCTATT 3632
    |||
Db 849 ACGTATTCATTTGTGTAATAATTAATTTATGTAACAACCTCTTACATTTGAATCTATT 908
QY 3633 TTTGCTCACTGATTCCTCATCTCTTGAAGTGAAGAGTGGAAAGCTAGGCCACAAT 3692
    |||
Db 909 TTTGCTCACTGATTCCTCATCTCTTGAAGTGAAGAGTGGAAAGCTAGGCCACAAT 968
QY 3693 TACGGCTCTGTGTGATTAAGATTTTACTGCAATTTTTCGATTTGCTTTT 3752
    |||
Db 969 TACGGCTCTGTGTGATTAAGATTTTACTGCAATTTTTCGATTTGCTTTT 1028
QY 3753 GGGCAAAACCTTACCTCCGCTAATATCAACTTTCCGTTCTGTACATTTGTCACAAA 3812
    |||
Db 1029 GGGCAAAACCTTACCTCCGCTAATATCAACTTTCCGTTCTGTACATTTGTCACAAA 1088
QY 3813 CCCTGAACCCCTAATCTTTCGCGGTGAGCTAGCCCTCCGCTTCTCTTCCACATTTCA 3872
    |||
Db 1089 CCCTGAACCCCTAATCTTTCGCGGTGAGCTAGCCCTCCGCTTCTCTTCCACATTTCA 1148
QY 3873 AAGTACCCCTGTATCTCAATTAATTAATCTTCACTTTAACTGTCTTTTTCGTTGCGCTC 3932
    |||
Db 1149 AAGTACCCCTGTATCTCAATTAATTAATCTTCACTTTAACTGTCTTTTTCGTTGCGCTC 1208
QY 3933 TTCCAACTCCCGCCCAAAATTCCTGTACGGGTAGCGACTTTGATTTATTTTCAAAAT 3992
    |||
Db 1209 TTCCAACTCCCGCCCAAAATTCCTGTACGGGTAGCGACTTTGATTTATTTTCAAAAT 1268
QY 3993 GTTTTCTCTTACAAACAACAAAAAGGTTTC 4025
    |||
Db 1269 GTTTTCTCTTACAAACAACAAAAAGGTTTC 1301

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RESULT 6

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US-09-234-186-5
; Sequence 5, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
; US-09-234-186-5

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Query Match          9.6%; Score 632.6; DB 4; Length 1315;
Best Local Similarity 99.8%; Pred. No. 5.9e-138;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 669 GGAGGACTTCATGACACTCGGAAAAACAATGANAAGAGACTACGACAGCAGAGCTGA 728
QY 3453 AAAAGTGGAGCGCGGAAAGCAGACAGAGCGGTGATGATGCGCTGGAGTAACAGC 3512
    |||
Db 729 AAAAGTGGAGCGCGGAAAGCAGACAGAGCGGTGATGATGCGCTGGAGTAACAGC 788
QY 3513 TGGAGCCATTGGAATCGTTGGAGTCTGCTGTGGGCGGATGATGTTCACTTGAAGTA 3572
    |||
Db 789 TGGAGCCATTGGAATCGTTGGAGTCTGCTGTGGGCGGATGATGTTCACTTGAAGTA 848
QY 3573 ACGTATTCATTTGTGTAATAATTAATTTATGTAACAACCTCTTACATTTGAATCTATT 3632
    |||
Db 849 ACGTATTCATTTGTGTAATAATTAATTTATGTAACAACCTCTTACATTTGAATCTATT 908
QY 3633 TTTGCTCACTGATTCCTCATCTCTTGAAGTGAAGAGTGGAAAGCTAGGCCACAAT 3692
    |||
Db 909 TTTGCTCACTGATTCCTCATCTCTTGAAGTGAAGAGTGGAAAGCTAGGCCACAAT 968
QY 3693 TACGGCTCTGTGTGATTAAGATTTTACTGCAATTTTTCGATTTGCTTTT 3752
    |||
Db 969 TACGGCTCTGTGTGATTAAGATTTTACTGCAATTTTTCGATTTGCTTTT 1028
QY 3753 GGGCAAAACCTTACCTCCGCTAATATCAACTTTCCGTTCTGTACATTTGTCACAAA 3812
    |||
Db 1029 GGGCAAAACCTTACCTCCGCTAATATCAACTTTCCGTTCTGTACATTTGTCACAAA 1088
QY 3813 CCCTGAACCCCTAATCTTTCGCGGTGAGCTAGCCCTCCGCTTCTCTTCCACATTTCA 3872
    |||
Db 1089 CCCTGAACCCCTAATCTTTCGCGGTGAGCTAGCCCTCCGCTTCTCTTCCACATTTCA 1148
QY 3873 AAGTACCCCTGTATCTCAATTAATTAATCTTCACTTTAACTGTCTTTTTCGTTGCGCTC 3932
    |||
Db 1149 AAGTACCCCTGTATCTCAATTAATTAATCTTCACTTTAACTGTCTTTTTCGTTGCGCTC 1208
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Db 1209 TTCACACTCCCCCAATTCCTGTACGCGTAGCGACTTGTATTTTTCACAAAT 1268
QY 3993 GTTTCTCTCTACACAAACAAAAAAGCGTTC 4025
Db 1269 GTTTCTCTCTACACAAACAAAAAAGCGTTC 1301

RESULT 7

US-09-234-186-6
; Sequence 6, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; EARLIER FILING DATE: 1999-01-20
; EARLIER FILING DATE: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER FILING DATE: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-234-186-6

Query Match 9.6%; Score 632.6; DB 4; Length 1315;
Best Local Similarity 99.8%; Pred. No. 5,9e-138;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3393 GGAGACTTCTGACACTCGGAAAAAATGAAGAGACTAGCAAGACAGAGAGCTGA 3452
Db 669 GGAGACTTCTGACACTCGGAAAAAATGAAGAGACTAGCAAGACAGAGAGCTGA 728
QY 3453 AAAGTGGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3512
Db 729 AAAGTGGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 788
QY 3513 TGGAGCCATTGGAAATCGTTGGAGTGTGTGTGGCGGATGATGTTAGCTGAAGA 3572
Db 789 TGGAGCCATTGGAAATCGTTGGAGTGTGTGTGGCGGATGATGTTAGCTGAAGA 848
QY 3573 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3632
Db 849 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
QY 3633 TTTGCTCACTGATTTCTCATCTTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAG 3692
Db 909 TTTGCTCACTGATTTCTCATCTTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAG 968
QY 3693 TAGGGCTCTGTGTGATTTAGATTTTATGTCGAATTTTTCGATTTGCTTTT 3752
Db 969 TAGGGCTCTGTGTGATTTAGATTTTATGTCGAATTTTTCGATTTGCTTTT 1028
QY 3753 GGGCAAAACCTACTTCGCGTATATCAACTTTTCGTTGTTGTTGTTGTTGTTGTT 3812
Db 1029 GGGCAAAACCTACTTCGCGTATATCAACTTTTCGTTGTTGTTGTTGTTGTTGTT 1088
QY 3813 CCTGAAACCTTAATTTTCTGCGCGTGTAGCCTCCCGCTTCTCTCAACATTTCA 3872

Db 1089 CCTGAAACCTTAATTTTCTGCGCGTGTAGCCTCCCGCTTCTCTCAACATTTCA 1148
QY 3873 AAGTACCCTGTATCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3932
Db 1149 AAGTACCCTGTATCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1208
QY 3933 TTCCACTCCCGCAATTCCTGTACGCGTAGCGAGATTTGATTTTATTTTCAAAAT 3992
Db 1209 TTCCACTCCCGCAATTCCTGTACGCGTAGCGAGATTTGATTTTATTTTCAAAAT 1268
QY 3993 GTTTCTCTCTACACAAACAAAAAAGCGTTC 4025
Db 1269 GTTTCTCTCTACACAAACAAAAAAGCGTTC 1301

RESULT 8

US-09-233-527-2
; Sequence 2, Application US/09233527
; Patent No. 6465617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09/233,527
; EARLIER FILING DATE: 1999-01-20
; EARLIER FILING DATE: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER FILING DATE: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-233-527-2

Query Match 9.6%; Score 632.6; DB 4; Length 1315;
Best Local Similarity 99.8%; Pred. No. 5,9e-138;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3393 GGAGACTTCTGACACTCGGAAAAAATGAAGAGAGACTAGCAAGAGAGAGCTGA 3452
Db 669 GGAGACTTCTGACACTCGGAAAAAATGAAGAGAGACTAGCAAGAGAGAGAGCTGA 728
QY 3453 AAAGTGGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3512
Db 729 AAAGTGGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 788
QY 3513 TGGAGCCATTGGAAATCGTTGGAGTGTGTGTGGCGGATGATGTTAGCTGAAGA 3572
Db 789 TGGAGCCATTGGAAATCGTTGGAGTGTGTGTGGCGGATGATGTTAGCTGAAGA 848
QY 3573 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3632
Db 849 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
QY 3633 TTTGCTCACTGATTTCTCATCTTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAG 3692
Db 909 TTTGCTCACTGATTTCTCATCTTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAG 968
QY 3693 TAGGGCTCTGTGTGATTTAGATTTTATGTCGAATTTTTCGATTTGCTTTT 3752

Db 969 TACGGCTCTCTGTCTGATTTACGATTTTACTGCAATTTTTCOCATTCGCTTTT 1028
QY 3753 GGGCAAAACCTTACTTCCGGTAATATCACTTTCCGTCTGTACATTTGCTCAAAA 3812
Db 1029 GGGCAAAACCTTACTTCCGGTAATATCACTTTCCGTCTGTACATTTGCTCAAAA 1088
QY 3813 CCGTGAACCTTACTTCTTCCGCGGTACGCTTCCGCTCTCTCCATTTTCA 3872
Db 1089 CCGTGAACCTTACTTCTTCCGCGGTACGCTTCCGCTCTCTCCATTTTCA 1148
QY 3873 AAGTACCCCTGTATCTCAATATTTACTTACTGTCTCTTTCTGTGGCCTC 3932
Db 1149 AAGTACCCCTGTATCTCAATATTTACTTACTGTCTCTTTCTGTGGCCTC 1208
QY 3933 TTCCAACTCCCGCAATTTCTGTACGCGGACGCTTTGATTTATTTTTCAAAT 3992
Db 1209 TTCCAACTCCCGCAATTTCTGTACGCGGACGCTTTGATTTATTTTTCAAAT 1268
QY 3993 GTTTTCTCTCTACACACAAAAAAGGCTC 4025
Db 1269 GTTTTCTCTCTACACACAAAAAAGGCTC 1301

RESULT 9
US-09-233-527-4
; Sequence 4, Application US/09233527
; Patent No. 6465617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09/233,527
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-233-527-4

Query Match 9.6%; Score 632.6; DB 4; Length 1315;
Best Local Similarity 99.8%; Pred. No. 5.9e-138;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3393 GGACGACTTCTGACACTCGGAAAAAACAATGAAAGAGACTACGACAGAGAGAGCTGA 3452
Db 669 GGACGACTTCTGACACTCGGAAAAAACAATGAAAGAGACTACGACAGAGAGAGCTGA 728
QY 3453 AAAAGTGGAGCGCGGAG 3512
Db 729 AAAAGTGGAGCGCGGAG 788
QY 3513 TGGACCATTTGGAATCTGTGAGTCTGTGTGGCGGAGATGATGTTCACTTGAAGTA 3572
Db 789 TGGACCATTTGGAATCTGTGAGTCTGTGTGGCGGAGATGATGTTCACTTGAAGTA 848
QY 3573 ACGTATTCATTTGTGTAATTAATTATTTATGTAACAATCTTACATTTGAATCTCAT 3632
Db 3632 ACGTATTCATTTGTGTAATTAATTATTTATGTAACAATCTTACATTTGAATCTCAT 3632

Db 849 ACGTATTCATTTGTGTAATTAATTATTTATGTAACAATCTTACATTTGAATCTCAT 908
QY 3633 TTGGTCACTGATCTGTCATCTTGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3692
Db 909 TTGGTCACTGATCTGTCATCTTGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 968
QY 3693 TACGGCTCTCTGTCTGATTTACGATTTTACTGCAATTTTTCOCATTCGCTTTT 3752
Db 969 TACGGCTCTCTGTCTGATTTACGATTTTACTGCAATTTTTCOCATTCGCTTTT 1028
QY 3753 GGGCAAAACCTTACTTCCGGTAATATCACTTTCCGTCTGTACATTTGCTCAAAA 3812
Db 1029 GGGCAAAACCTTACTTCCGGTAATATCACTTTCCGTCTGTACATTTGCTCAAAA 1088
QY 3813 CCGTGAACCTTACTTCTTCCGCGGTACGCTTCCGCTCTCTCCATTTTCA 3872
Db 1089 CCGTGAACCTTACTTCTTCCGCGGTACGCTTCCGCTCTCTCCATTTTCA 1148
QY 3873 AAGTACCCCTGTATCTCAATATTTACTTACTGTCTCTTTCTGTGGCCTC 3932
Db 1149 AAGTACCCCTGTATCTCAATATTTACTTACTGTCTCTTTCTGTGGCCTC 1208
QY 3933 TTCCAACTCCCGCAATTTCTGTACGCGGACGCTTTGATTTATTTTTCAAAT 3992
Db 1209 TTCCAACTCCCGCAATTTCTGTACGCGGACGCTTTGATTTATTTTTCAAAT 1268
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Db 1269 GTTTTCTCTCTACACACAAAAAAGGCTC 1301

RESULT 10
US-09-233-527-5
; Sequence 5, Application US/09233527
; Patent No. 6465617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09/233,527
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-233-527-5

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Best Local Similarity 99.8%; Pred. No. 5.9e-138;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 669 GGACGACTTCTGACACTCGGAAAAAACAATGAAAGAGACTACGACAGAGAGAGCTGA 728
QY 3453 AAAAGTGGAGCGCGGAG 3512
Db 3512 AAAAGTGGAGCGCGGAG 788

Matches	632:	Conservative	1:	Mismatches	0:	Indels	0:	Gaps	0:
QY	3393	GGACACATCTCATGACACTCTGGAAAAACAATGAAGAGAGACTTACGAACGAGCAGACACTGA	3452						
Db	669	GGACACATCTCATGACACTCTGGAAAAACAATGAAGAGAGACTTACGAACGAGCAGACACTGA	728						
QY	3453	AAAAATGGGAGCCGGGAAGCAGAACACAGCGGTGGTCATATGATGGCGCTGGAGTAACGC	3512						
Db	729	AAAAATGGGAGCCGGGAAGCAGAACACAGCGGTGGTCATATGATGGCGCTGGAGTAACGC	788						
QY	3513	TGGAGCCATTGGAAATCGTTGGAGTCGTGCTGTGTGGCGGAGATGATGTCAGCTTGAAGTA	3572						
Db	789	TGGAGCCATTGGAAATCGTTGGAGTCGTGCTGTGTGGCGGAGATGATGTCAGCTTGAAGTA	848						
QY	3573	ACGTAATCAATTTGTSTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	3632						
Db	849	ACGTAATCAATTTGTSTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	908						
QY	3633	TTTGTCTACGATTTCTCTCAATCTTTGAACCTGGAAAGACTGGAAAAAGCTAGGCCACAAT	3692						
Db	909	TTTGTCTACGATTTCTCTCAATCTTTGAACCTGGAAAGACTGGAAAAAGCTAGGCCACAAT	968						
QY	3693	TACGGCTCTGTGTGAGTATTACGATTTTACGCAATTTTTCGCATTTCCCTTTT	3752						
Db	969	TACGGCTCTGTGTGAGTATTACGATTTTACGCAATTTTTCGCATTTCCCTTTT	1028						
QY	3753	GGCCAAACCTTACTTCGCGTAATATCAACTTTCCGTGCTGTGACATTTTCGTCAAAAA	3812						
Db	1029	GGCCAAACCTTACTTCGCGTAATATCAACTTTCCGTGCTGTGACATTTTCGTCAAAAA	1088						
QY	3813	CCCTGAAACCCCTTACTTTCTCGCGGTGGCCCTAGCGCTCCGCTCTCTCCACATTTTCCA	3872						
Db	1089	CCCTGAAACCCCTTACTTTCTCGCGGTGGCCCTAGCGCTCCGCTCTCTCCACATTTTCCA	1148						
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PCT-US93-05651-2									
Sequence 2, Application PC/TUS9305651									
GENERAL INFORMATION:									
TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death									
NUMBER OF SEQUENCES: 5									
COMPUTER READABLE FORM:									
MEDIUM TYPE: diskette									
CURRENT APPLICATION DATA:									
APPLICATION NUMBER: PCT/US93/05651									
INFORMATION FOR SEQ ID NO: 2:									
SEQUENCE CHARACTERISTICS:									
LENGTH: 1315 base pairs									
TYPE: nucleic acid									
STRANDEDNESS: double									
TOPOLOGY: linear									
MOLECULE TYPE: cDNA to mRNA									
FEATURE:									
NAME/KEY: CDS									
LOCATION: 7..846									
OTHER INFORMATION: /product= "Ced-9"									

FILED DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3920001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7653 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: join(2232..2366, 2430..2576, 2855..3109, 4305
LOCATION: ..4634, 5547..5759, 5817..5942, 6298..6537, 7012
LOCATION: ..7075)
US-08-258-287B-1

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Best Local Similarity 73.3%; Pred. No. 9.5e-23;
Matches 211; Conservative 0; Mismatches 63; Indels 14; Gaps 2;

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DB 1635 TGAATATTATTCGGAACACAAATTCAGAGATGCGTATTACAGTCATATTGGCGGC 1576
QY 3123 AAAATATCCAGTAGAGAAACTACAGTAATCTTTAAAT-----TTTAAATTTTAC 3176
DB 1575 AAAATATCTCGTAGCTACAGTAATCTTTAAATGACTCTAGCGCTTGACG 1516
QY 3177 AATTAAAGAAATTAACCACTAATCAAAAGAAATTAATTTCAAAATCGAGCCGTAATC 3236
DB 1515 AATTACGGGTATCAAAATTCGAAAAATTAATTTCAAAATGAGCCGTAATC 1456
QY 3237 GA-----CTACAGTAGGATTTAAAGATTTACTGAGTTTCGCTACAGATATTTC 3288
DB 1455 GACACAAGCGCTACAGTAGTCAATTTAAAGAAATTTGAGTTTCGCTACAGATATTTC 1396
QY 3289 CGCCTCAAAATATGTTGAAATACGATTCACGAGTTTGTGTTCC 3336
DB 1395 GCCGTCAAAATATGTTGCGCAGTACGATTCACGATTTTGTGATTC 1348

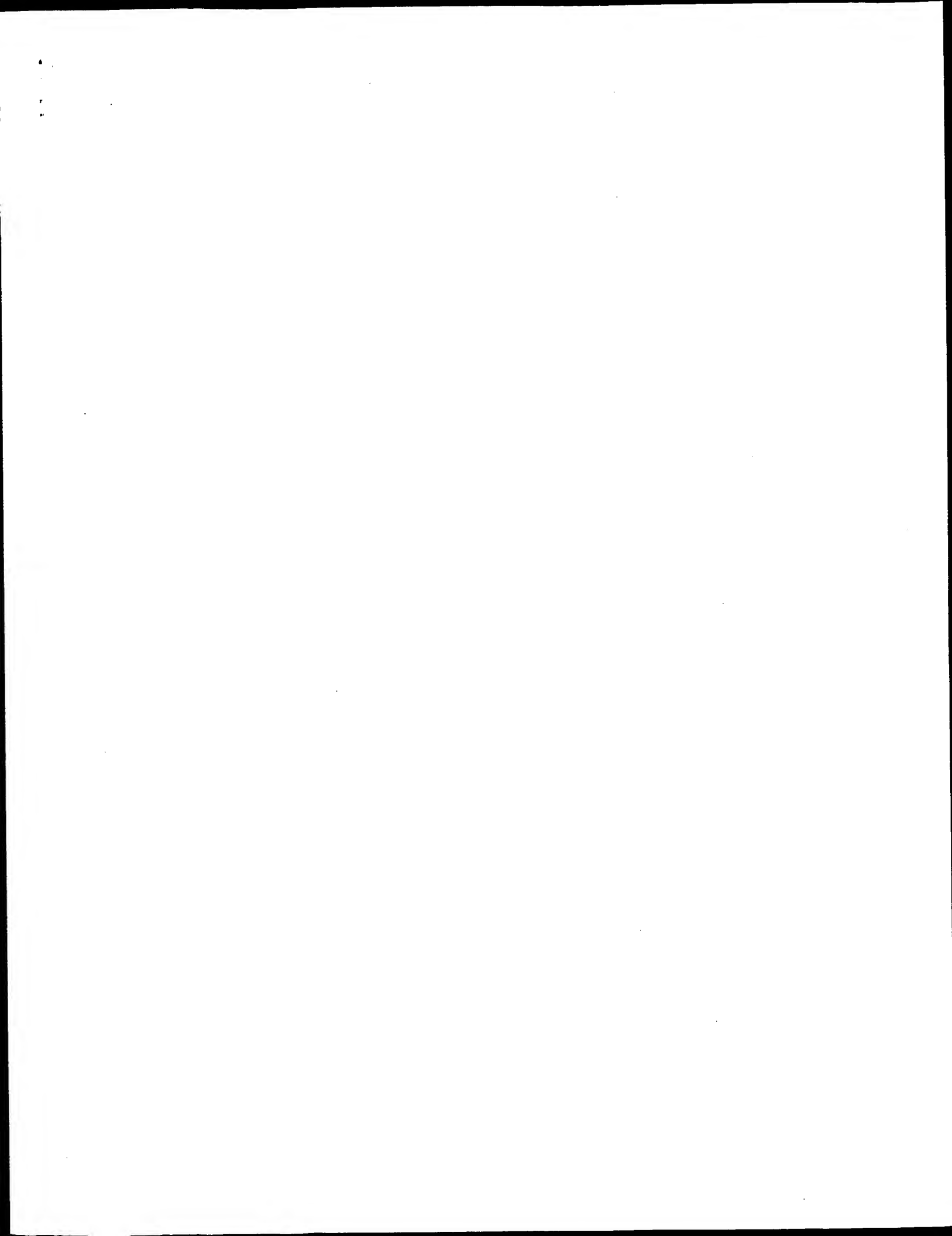
RESULT 15
US-08-368-704C-1/c
Sequence 1, Application US/08368704C
Patent No. 6087160
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/368,704C
FILING DATE: 4-JAN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/258,287
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3920002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7653 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: join(2232..2366, 2430..2576, 2855..3109, 4305
LOCATION: ..4634, 5547..5759, 5817..5942, 6298..6537, 7012
LOCATION: ..7075)
US-08-368-704C-1

Query Match 2.1%; Score 139.2; DB 3; Length 7653;
Best Local Similarity 73.3%; Pred. No. 9.5e-23;
Matches 211; Conservative 0; Mismatches 63; Indels 14; Gaps 2;

QY 3063 TGTATTGTTACGGAATACAAATTCGCAATGCTATTTCACACATATTGACGGC 3122
DB 1635 TGAATATTATTCGGAACACAAATTCAGAGATGCGTATTACAGTCATATTGGCGGC 1576
QY 3123 AAAATATCCAGTAGAGAAACTACAGTAATCTTTAAAT-----TTTAAATTTTAC 3176
DB 1575 AAAATATCTCGTAGCTACAGTAATCTTTAAATGACTAGTACGCTTGACG 1516
QY 3177 AATTAAAGAAATTAACCACTAATCAAAAGAAATTAATTTCAAAATCGAGCCGTAATC 3236
DB 1515 AATTACGGGTATCAAAATTCGAAAAATTAATTTCAAAATGAGCCGTAATC 1456
QY 3237 GA-----CTACAGTAGGATTTAAAGATTTACTGAGTTTCGCTACAGATATTTC 3288
DB 1455 GACACAAGCGCTACAGTAGTCAATTTAAAGAAATTTGAGTTTCGCTACAGATATTTC 1396
QY 3289 CGCCTCAAAATATGTTGAAATACGATTCACGAGTTTGTGTTCC 3336
DB 1395 GCCGTCAAAATATGTTGCGCAGTACGATTCACGATTTTGTGATTC 1348

Search completed: February 28, 2003, 04:35:12
Job time : 366.757 secs



GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using SW model

Run on: February 28, 2003, 03:32:51 ; Search time 651.418 Seconds
(without alignments)
6280.048 Million cell updates/sec

Title: US-09-993-420A-1

Perfect score: 6560
Sequence: 1 atcgatagtcgtccacaaat.....gtttgataaaatataca 6560

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 460893 seqs, 311809382 residues

Total number of hits satisfying chosen parameters: 921786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139.2	2.1	7653	10	US-09-888-243-1
2	101.8	1.6	7653	10	US-09-888-243-1
3	93	1.4	4560	10	US-09-945-258-11
4	79.8	1.2	4560	10	US-09-945-258-11
5	68.6	1.0	29793	9	US-09-973-451-38
6	67.6	1.0	25002	9	US-10-024-623-31
7	64.6	1.0	25002	9	US-10-024-623-31
8	63.4	1.0	29793	10	US-09-973-451-38
9	56	0.9	2000	9	US-09-938-842A-4849
10	53	0.8	416	10	US-09-960-352-4584
11	52.2	0.8	404	10	US-09-960-352-4144
12	51.6	0.8	2773	9	US-09-992-598-178
13	51.6	0.8	2773	9	US-09-989-293A-178
14	51.6	0.8	2773	9	US-10-063-547-33
15	51.6	0.8	2773	9	US-09-989-735-178
16	51.6	0.8	2773	9	US-09-990-444-178
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19	51.6	0.8	2773	9	US-09-991-181-178

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21	51.6	0.8	2773	9	US-09-989-734-178	Sequence 178, App
22	51.6	0.8	2773	9	US-09-997-633-178	Sequence 178, App
23	51.6	0.8	2773	9	US-10-174-590-149	Sequence 149, App
24	51.6	0.8	2773	9	US-10-176-758-149	Sequence 149, App
25	51.6	0.8	2773	9	US-10-063-616-33	Sequence 33, App1
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ALIGNMENTS

RESULT 1
US-09-888-243-1/c
Sequence 1, Application US/09888243
Patent No. US20020136714A1
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Yuan, Junyang
APPLICANT: Shih, Shai
TITLE OF INVENTION: Relatedness of Human Interleukin-1beta
TITLE OF INVENTION: Convertase Gene to a C. Elegans Cell Death Gene, Inhibitory
FILE REFERENCE: 01997/211003
CURRENT APPLICATION NUMBER: US/09/888,243
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 09/083,662
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: US 08/394,189
PRIOR FILING DATE: 1995-02-24
PRIOR APPLICATION NUMBER: US 08/282,211
PRIOR FILING DATE: 1994-07-11
PRIOR APPLICATION NUMBER: US 07/984,182
PRIOR FILING DATE: 1992-11-20
PRIOR APPLICATION NUMBER: US 07/897,788
PRIOR FILING DATE: 1992-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Fastseq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 7653
TYPE: DNA
ORGANISM: Caenorhabditis elegans
US-09-888-243-1
Query Match 2.1%; Score 139.2; DB 10; Length 7653;
Best Local Similarity 73.3%; Pred. No. 3.9e-18;
Matches 211; Conservative 0; Mismatches 63; Indels 14; Gaps 2;
QY 3063 TGTATTGTTACGGGAATACAAATTCGACGAATGCTATTTCACACATATTGACCGC 3122
DB 1635 TGAATTTTACGGGAACAAATTCGACGAATGCTATTTCACATATTGACCGC 1576
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Db 1515 AATTACGGGTATCCAAAATTCGAAAAAATAATTTTCAAAAAATGAGCCCGTAATC 1456

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Db 1455 GACACAAAGCGGTACAGTACGATTTTAAAGAAATACGTGTAAGTTTGCTACGAGATATTTT 1356

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RESULT 2
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: Sequence 1: Application US/09888243
: Patent No. US20020136714A1
: GENERAL INFORMATION:
: APPLICANT: Horvitz, H. Robert
: APPLICANT: Yuan, Junying
: APPLICANT: Shaham, Shai
: TITLE OF INVENTION: Relatedness of Human Interleukin-1beta
: TITLE OF INVENTION: Convertase Gene to a C. Elegans Cell Death Gene, Inhibitory
: TITLE OF INVENTION: Portions of these Genes and Uses Therefor
: FILE REFERENCE: 01997/211003
: CURRENT APPLICATION NUMBER: US/09/888, 243
: CURRENT FILING DATE: 2001-06-22
: PRIOR APPLICATION NUMBER: US 09/083, 662
: PRIOR FILING DATE: 1998-05-22
: PRIOR APPLICATION NUMBER: US 08/394, 189
: PRIOR FILING DATE: 1995-02-24
: PRIOR APPLICATION NUMBER: US 08/282, 211
: PRIOR FILING DATE: 1994-07-11
: PRIOR APPLICATION NUMBER: US 07/984, 182
: PRIOR FILING DATE: 1992-11-20
: PRIOR APPLICATION NUMBER: US 07/897, 788
: PRIOR FILING DATE: 1992-06-12
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 7653
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
US-09-888-243-1

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[illegible]

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US-09-945-258-11/c
? Sequence 11, Application US/09945258
? Patent No. US20020058276A1
? GENERAL INFORMATION:
? APPLICANT: St.George-Hyslop, Peter H.
? APPLICANT: Fraser, Paul E.
? APPLICANT: University of Toronto
? TITLE OF INVENTION: PROTEINS RELATED TO SCHIZOPHRENIA AND USES THEREOF
? FILE REFERENCE: 1034/11570
? CURRENT APPLICATION NUMBER: US/09/945,258
? CURRENT FILING DATE: 2001-08-31
? PRIOR APPLICATION NUMBER: US 60/229,889
? PRIOR FILING DATE: 2000-09-01
? NUMBER OF SEQ ID NOS: 19
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 11
? LENGTH: 4560
? TYPE: DNA
? ORGANISM: C. Elegans
US-09-945-258-11

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Best Local Similarity	72.4%	Pred. No. 5e-09:		
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DB	4244	GAAATTTTGTAAATTCGAAAAAGGTGGCCCTTTAAAGAAATACGTATTTCTTGCACT	4185	
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Db	3919	TTTCGATTAAAGAAACTACATTT-1GAATCAAGTTTTCTTAATCTTTAGACAAATTATAC	397777
Qy	4664	CCAAACGTTCTTTACACGAAATTTTGCATTTTGGATTAATACGATACCTGGTCC	4723
Db	3978	TCACATTTGATGCCCGACGAAAGTTTGGCATTTTGAGCCAAAACGCGTGCCAGGTCC	4037
Qy	4724	GACACGAACATTTTGTAAATTCAAAAAGATGTGCAGCTTTAAAGAGTGTAGATT	4783
Db	4038	GACACGAAAAATTATTTATTTGAAAAATATGTTTTGCCCTTTAAATGTAAGTACTGATTTT	4097
Qy	4784	GAAACTTCGTGTGGTGGAGATT	4806
Db	4098	CGAATTCATGCTGCGCATTT	4120

RESULT 5
 US-09-973-451-38
 : Sequence 38, Application US/09973451
 : Patent No. US20020132328A1
 : GENERAL INFORMATION:
 : APPLICANT: JACOBSON, Myron K.
 : APPLICANT: JACOBSON, Elaine L.
 : APPLICANT: AM, Jean-Christophe
 : APPLICANT: LIN, Winston
 : TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE
 : TITLE OF INVENTION: (PARC) ENZYMES,
 : TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
 : FILE REFERENCE: NTAD 201
 : CURRENT APPLICATION NUMBER: US/09/973,451
 : CURRENT FILING DATE: 2001-10-09
 : PRIOR APPLICATION NUMBER: US/09/302,812
 : PRIOR FILING DATE: 1999-04-30
 : PRIOR APPLICATION NUMBER: 60/083,768
 : PRIOR FILING DATE: 1998-05-01
 : NUMBER OF SEQ ID NOS: 38
 : SEQ ID NO 38
 : LENGTH: 29793
 : TYPE: DNA
 : ORGANISM: *Caenorhabditis elegans*
 : FEATURE:
 US-09-973-451-38

	Query Match	1.0%	Score 68.6	DB 10	Length 29793
	Best Local Similarity	68.6%	Pred. No. 0.00076		
	Matches 109	Conservative 0	Mismatches 49	Indels 1	Gaps 14
QY	4683	AAATTTGCGATTTTTCAGCTTAAATACGATACCGCTGTCGACACGAAACATTTTGGT	4742		
Db	5611	ATTTTCATATTTGTGATGCAAAAATACGATACCGGATCTTGATACATACCA-ATTTTGTGA	5669		
QY	4743	AAATTCAAAAGATGTGGCCCTTTAAAGAGTGTCTGTAGTTGAAACTTCGTTGTGGCG	4802		
Db	5670	AAATGCGAAAAGGTTCGACCTTTAAAAAGAACTGCAATTTCAAAACACTGTGTGGTGG	5729		
QY	4803	ACCTTCATCGATTTTTCGTACGCTTTTATATAAGAAA	4841		
Db	5730	ATGTGTTATGCGTTTATATTTTTCGTAGAGGTAAA	5768		

```

RESULT 6
US-10-024-623--31
: Sequence 31, Application US/10024623
: Publication No. US20020187524A1
: GENERAL INFORMATION:
: APPLICANT: CURTIS, RORY A.J.
: TITLE OF INVENTION: 8039, 46455, 54414, 53763, 67076, 67102, 44181,
: TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
: TITLE OF INVENTION: USE THEREOF
: FILE REFERENCE: MNI-214CP
: CURRENT APPLICATION NUMBER: US/10/024,623
: CURRENT FILING DATE: 2001-12-17

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; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ. ID NOS.: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 25002
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-10-024-623--31

```

Query Match	1.0%;	Score 67.6;	DB 9;	Length 25002;
Best Local Similarity	64.9%;	Pred. No. 0.0011;		
Matches 100; Conservative	0;	Mismatches 54;	Indels 0;	Gaps 0;

QY	3328	ACACACATATAGCATTTAAAGATTTACTGATTTTCCGTACAGAAATTTTTCCGCCTCAAA	3297
Db	2278	AGTACAAAGTCATTAATAATTGTTTAAATTTCCGTACAGATATTTCCGGGTCAAA	22847
QY	328	TATTTGTGAAATATAGCATTTCCAGATTTTGTCTCCCGAATATGCTCTAAGCAT	3357
Db	22848	TATTTTCCGCAATACGCATTTTCCAAACGTAGTGTCTGTATTAATTATGTTTCATTTCT	22907
QY	3358	ATTTTGTGAAATATTAATAATCAAGAAAAAATATTC	3391
Db	22908	GCTTCAAAAAGCTAATATTTTATTTATTCAGTAGC	22941

```

RESULT 7
US-10-024-623-31/c
: Sequence 31, Application US/10024623
: Publication No. US20020187524A1
: GENERAL INFORMATION:
: APPLICANT: Curtis, Rory A.J.
: TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181,
: TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
: FILE REFERENCE: NM1-214CP
: CURRENT APPLICATION NUMBER: US/10/024,623
: CURRENT FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: US 60/256,240
: PRIOR FILING DATE: 2000-12-15
: PRIOR APPLICATION NUMBER: US 60/256,588
: PRIOR FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: US 60/258,028
: PRIOR FILING DATE: 2000-12-21
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 31
: LENGTH: 25002
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
US-10-024-623-31

```

Query Match	1.0%;	Score 64.6;	DB 9;	Length 25002;
Best Local Similarity	68.7%;	Pred. No. 0.0044;		
Matches 103; Conservative	0;	Mismatches 42;	Indels 5;	Gaps 1

QY	6129	AACCTGATCAAGAGAGCTCTTAAAGATATACGTGATTTGGCAGACGAGT-----A	6183
Db	22393	AAACGAGTCTACGGTAGTCATCTAAAAAGTGGCTGATTTTGGCGTACCGTACAAATCA	22333
QY	6184	TTTTGNGNGCAATATGTTGGGCAATACGATCTCTAGAAATGTGTGTTCTCTGTAATGT	6243
Db	22333	TTTTTCGCGTCAATATATGTTGGCAATACGCACTTTCTAGTATTAAGTGTTCGCCGTAATAT	22274
QY	6244	CTTGAATAATTTTCCATTTTCACATCAATAA	6273
Db	22273	TTATATTTTATTTACTATTTAGAAAAAAA	22244

```
RESULT 8
US-09-973-451-38/c
: Sequence 38, Application US/09973451
: Patent No. US20020132328A1
: GENERAL INFORMATION:
: APPLICANT: JACOBSON, Myron K.
: APPLICANT: JACOBSON, Elaine L.
: APPLICANT: AM, Jean-Christophe
: APPLICANT: LIN, Winston
: TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOPHROLASE
: TITLE OF INVENTION: (PARC) ENZYMS, AND ANTIBODIES IMMUNOREACTIV
: TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
: FILE REFERENCE: NIAD 201
: CURRENT APPLICATION NUMBER: US/09/973,451
: PRIOR FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: US/09/302,812
: PRIOR FILING DATE: 1999-04-30
: PRIOR APPLICATION NUMBER: 60/083,768
: PRIOR FILING DATE: 1998-05-01
: NUMBER OF SEQ ID NOS: 38
: SEQ ID NO 38
: LENGTH: 29793
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
: FEATURE:
US-09-973-451-38

Query Match
Best Local Similarity 1.08; Score 63.4; DB 10; Length 29793;
Matches 82; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 4676 TACAGCAATTTTCGATTTTTCGATTTTAAATACGATACCTGCTGCACAGCAAAAT 4735
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5914 TATGTGAATTTTTCACATTTTAAATGCAAAATCAGGTACCGGTTTCGACGACAAAT 5855
QY 4736 TTTTGTAAATTCAAAAAGATGCGCCCTTAAAGAGTGTGATTTGAAC 4788
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5854 GTTGTATATACAAATGATGTCGCTTTGAAAAGTACTGATTCCAATC 4802

RESULT 9
US-09-938-842A-4849
: Sequence 4849, Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kieps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: TITLE OF INVENTION: SAME, AND METHODS OF USE
: FILE REFERENCE: SCRIPI300-3
: CURRENT APPLICATION NUMBER: US/09/938,842A
: PRIOR FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227,866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 4849
: LENGTH: 2000
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-4849

Query Match
Best Local Similarity 0.9%; Score 56; DB 9; Length 2000;
Matches 155; Conservative 0; Mismatches 145; Indels 2; Gaps 1;
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QY 2366 TCTTTTGGAAAGTTTTCATTAAAAACACGAAATTTGATCCGGATGTAAATTTT 2425
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1517 TTTAATTTTACAAATTTTCAAAATATACCGAATTTTAAATCGATTAATTAAT 1576
QY 2426 TTGTGATTAATTTACGAAACTTTACGAATTCATTAATAAAGCTATTTTCTATTCGA 2485
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1577 AATTTTCAAAAAAACAACGACATTTAAAAAATATATTAATCAATCATTAATATTA 1636
QY 2486 ATATTTTAAACCATATTTTCCTGATTTGATTTTCGAAAAAGATTCGATTAATCA 2545
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1637 ATTTTGTATTTATATATTTT--TTTATACCTTAACATTAATATATTCATATTTACT 1694
QY 2546 AAAATCGTTTTTAAATGTAATTTTGGAATAATACATTAATTCGATTTTGAACTT 2605
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1695 TAAAGTTTCAAAATTAATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1754
QY 2606 TTTTCTGAAAAACAGTTTTTTCGATTTGCTGACGAAAAACCCCAAAATTCAA 2665
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1755 AACTTTTGAACAAATTTTTCCTTTGAAAAATTAATTAATTAATTAATTAATTAAT 1814
QY 2666 TT 2667
    ||
DB 1815 TT 1816

RESULT 10
US-09-960-352-4584/c
: Sequence 4584, Application US/09960352
: Patent No. US20020137139A1
: GENERAL INFORMATION:
: APPLICANT: Warren, Wesley C.
: APPLICANT: Tao, Nengbing
: APPLICANT: Byatt, John C.
: APPLICANT: Mathalagan, Nagappan
: TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
: TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
: FILE REFERENCE: 16511.006/37-21(10298)C
: CURRENT APPLICATION NUMBER: US/09/960,352
: PRIOR FILING DATE: 2001-09-24
: NUMBER OF SEQ ID NOS: 15112
: SEQ ID NO 4584
: LENGTH: 416
: TYPE: DNA
: ORGANISM: Bos taurus
: OTHER INFORMATION: Clone ID: 20-LTB3057-016-Q1-K1-E11
US-09-960-352-4584

Query Match
Best Local Similarity 0.8%; Score 53; DB 10; Length 416;
Matches 179; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

QY 2303 AAAAATGTTTGTTCCTTCAGAAATCAGCAAACTTGCAAAATATGCCAATAT 2362
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 412 AAAATTTTGTTTTAAATTAATAATTTTATATTAATAATTTTATTAATTAATAATTC 353
QY 2363 GTGTCTTTTGAAGTTTTCATTAATAAACACGAAATTTGATCCGGAATGTAATTT 2422
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 352 CATATATTTTAAATATTTATTTAAATCTTTTATATCTCTTAATTTAAATTTAA 293
QY 2423 TTTTGTGATTAATTTACGAAACTTACGAATTCATTAATAAAGCTATTTTCTATT 2482
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 292 AATTTTAAATTTTAAATAATTTTCTTTAAATAATTTAAATTTTAAATTTTAAATTT 233
QY 2483 CGAATATTTTAAACATATTTTCCTGATTTGATTTTCGAAAAAGATTCGATTA 2542
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 232 TTTTGTATGCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 173
QY 2543 TCAAAAATCGTTTTTAAATGTAATAATTTTGGAATAATACATTAATAATTCATTTTGAA 2602
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 172 TTTTGTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 113
QY 2603 CTTTTCCTGCAAAACAGTTTTCGTCGATTTGCTGAACGAAAAACCCCAAAATTT 2662
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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D_b 112 TGCATTTTTCATTAAATTTTTTTTTTTTAAAAAAAATAAAAAAAAAATACCAAAACC 53
QY 2663 CAATTTTCGACATTAAAAACGAAAAA 2691
 || || ||||| |||||
D_b 52 AAAAAAATTAATAAAAAAAAAAAAAAAAAA 24

```

RESULT 11
US-09-960-352-4144
; Sequence 4144, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Ningbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(102981C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4144
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (155)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 18-LIB3038-042-Q1-K1-E9
US-09-960-352-4144

```

Query Match	0.8%	Score 52.2	DB 10	Length 404
Best Local Similarity	62.8%	Pred. No. 0.25		
Matches	81	Conservative	0	Mismatches 48; Indels 0; Gaps 0
QY	477	CGATGCATCAGAAATTCGAGAAATTTTGAATTCATCTTCGAAATTTGCAATGCAAAAAAT	536	
Db	253	CTATTATTTGTACGCAATCATCATTAATTTGTATTATATTCTAAAAA	312	
QY	537	AATTATTCAGAGAAATACAGAAATGCAACAAAAAACAAAAAAGACAAACA	596	
Db	313	AAA	372	
QY	597	AGTCGAAA	605	
Db	373	AAAAAAAAA	381	

US-09-992-598-178
 Sequence 178, Application US/09992596
 Patent No. US20020160384A1
 GENERAL INFORMATION
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Nupier, Mary A.
 APPLICANT: Poon, James
 APPLICANT: Rami, Nicholas F.
 APPLICANT: Roy, Margaret Ann

1 APPLICANT: Stewart, Timothy A.
 2 APPLICANT: Tumas, Daniel
 3 APPLICANT: Watanabe, Colin K.
 4 APPLICANT: Williams, P. Mickey
 5 APPLICANT: Wood, William I.
 6 APPLICANT: Zhang, Zemin
 7 TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
 8 TITLE OF INVENTION: Acids Encoding the Same
 9 FILE REFERENCE: P2730P1C20
 10 CURRENT APPLICATION NUMBER: US/09/992.598
 11 PRIOR APPLICATION NUMBER: 2001-11-14
 12 PRIOR FILING DATE: 1997-06-16
 13 PRIOR APPLICATION NUMBER: 60/062250
 14 PRIOR FILING DATE: 1997-10-17
 15 PRIOR APPLICATION NUMBER: 60/065166
 16 PRIOR FILING DATE: 1997-11-12
 17 PRIOR APPLICATION NUMBER: 60/065311
 18 PRIOR FILING DATE: 1997-11-13
 19 PRIOR APPLICATION NUMBER: 60/066770
 20 PRIOR FILING DATE: 1997-11-24
 21 PRIOR APPLICATION NUMBER: 60/075945
 22 PRIOR FILING DATE: 1998-02-25
 23 PRIOR APPLICATION NUMBER: 60/078910
 24 PRIOR FILING DATE: 1998-03-20
 25 PRIOR APPLICATION NUMBER: 60/083322
 26 PRIOR FILING DATE: 1998-04-28
 27 PRIOR APPLICATION NUMBER: 60/084600
 28 PRIOR FILING DATE: 1998-05-07
 29 PRIOR APPLICATION NUMBER: 60/087106
 30 PRIOR FILING DATE: 1998-05-28
 31 PRIOR APPLICATION NUMBER: 60/087607
 32 PRIOR FILING DATE: 1998-06-02
 33 PRIOR APPLICATION NUMBER: 60/087609
 34 PRIOR FILING DATE: 1998-06-02
 35 PRIOR APPLICATION NUMBER: 60/087759
 36 PRIOR FILING DATE: 1998-06-02
 37 PRIOR APPLICATION NUMBER: 60/087827
 38 PRIOR FILING DATE: 1998-06-03
 39 PRIOR APPLICATION NUMBER: 60/088021
 40 PRIOR FILING DATE: 1998-06-04
 41 PRIOR APPLICATION NUMBER: 60/088025
 42 PRIOR FILING DATE: 1998-06-04
 43 PRIOR APPLICATION NUMBER: 60/088026
 44 PRIOR FILING DATE: 1998-06-04
 45 PRIOR APPLICATION NUMBER: 60/088028
 46 PRIOR FILING DATE: 1998-06-04
 47 PRIOR APPLICATION NUMBER: 60/088029
 48 PRIOR FILING DATE: 1998-06-04
 49 PRIOR APPLICATION NUMBER: 60/088030
 50 PRIOR FILING DATE: 1998-06-04
 51 PRIOR APPLICATION NUMBER: 60/088033
 52 PRIOR FILING DATE: 1998-06-04
 53 PRIOR APPLICATION NUMBER: 60/088326
 54 PRIOR FILING DATE: 1998-06-04
 55 PRIOR APPLICATION NUMBER: 60/088167
 56 PRIOR FILING DATE: 1998-06-05
 57 PRIOR APPLICATION NUMBER: 60/088202
 58 PRIOR FILING DATE: 1998-06-05
 59 PRIOR APPLICATION NUMBER: 60/088212
 60 PRIOR FILING DATE: 1998-06-05
 61 PRIOR APPLICATION NUMBER: 60/088217
 62 PRIOR FILING DATE: 1998-06-05
 63 PRIOR APPLICATION NUMBER: 60/088655
 64 PRIOR FILING DATE: 1998-06-09
 65 PRIOR APPLICATION NUMBER: 60/088734
 66 PRIOR FILING DATE: 1998-06-10
 67 PRIOR APPLICATION NUMBER: 60/088738
 68 PRIOR FILING DATE: 1998-06-10
 69 PRIOR APPLICATION NUMBER: 60/088742
 70 PRIOR FILING DATE: 1998-06-10
 71 PRIOR APPLICATION NUMBER: 60/088610
 72 PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 0.8%; Score 51.6; DB 9; Length 2773;
Best Local Similarity 55.6%; Pred. No. 0.72; 79; Indels 0; Gaps 0;
Matches 99; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 428 AAGGTCATTTTGAAGCCGAAATTTTACTAAATCTCTAGCCATGAGTGCATGCAG 487
DB 2592 AAATTCATTTTGTGATGACATGTAGGAATTCGTAATTTAGAGATGAA 2651
QY 488 AAATTCGAGGAATTTAGATTTCTTGAATTTTCCAAATGAAAAATTAATTTCAA 547
DB 2652 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2711
QY 548 GAAATTCACAGAAATTCGAAACAAATTAATTAATTAATTAATTAATTAATTA 605
DB 2712 AA 2769

RESULT 13
US-09-989-293A-178
Sequence 178, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumus, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PIC66
 CURRENT APPLICATION NUMBER: US/09/989,293A
 PRIOR APPLICATION NUMBER: 2001-11-20
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-10-17
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 PRIOR FILING DATE: 1997-11-12
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 7 PRIOR APPLICATION NUMBER: 60/092182
 7 PRIOR FILING DATE: 1998-07-09

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Query Match          0.88;  Score 51.6;  DB 9;  Length 2773;
Best Local Similarity 55.68;  Pred. No. 0.72;
Matches 99;  Conservative 0;  Mismatches 79;  Indels 0;  Gaps 0;

QY 428 AAGCTCATTTTTCGAAGCCGAATTTTACTAAATCTCAGCCATGAGATCGATGATCAG 487
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Db 2592 AAGTTTCATTTTTCATGACATGATAGAGAAATGCTGAATTAATGTTAGAGAATGAA 2651

QY 488 AAAATTCGAGAAATTTTTCAGATTTTCATCTTGAATTTTGCAGTGAAGAAAAATTAATTATCAA 547
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2652 AAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2711

QY 548 GAAATATCAGAAAAATTCGACAAAAAACAATAAGACAAATGCGAAAA 605
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Db 2712 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2769

RESULT 14
US-10-063-547-33
: Sequence 33, Application US/10063547
: Publication No. US20020182638A1
: GENERAL INFORMATION:
: APPLICANT: Eaton, Dan L.
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3230R1C1
: CURRENT APPLICATION NUMBER: US/10/063,547
: CURRENT FILING DATE: 2002-05-02
: Prior application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 170

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: SEQ ID NO 33
: LENGTH: 2773
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-063-547-33

Query Match          0.8%; Score 51.6; DB 9; Length 2773;
Best Local Similarity 55.6%; Pred. No. 0.72; Mismatches 79; Indels 0; Gaps 0;
Matches 99; Conservative 0;

Oy 428 AAGGTCATTTTTCGAAGCCGCAATTTTACTAAATCTCTAGCCATGAGCTGATGATCAG 487
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Db 2552 AAGTTCATTTTTCGCAACAGACATCTAGCAATTTGCTGATTAATGTTAGAGCATGAA 2651

Oy 488 AATTCGAGGAATTTTACATTTTCATCTTGAATTTTGCATGGAATTAATTAATTCAAA 547
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Db 2652 AATTCGAGGAATTTTACATTTTCATCTTGAATTTTGCATGGAATTAATTAATTCAAA 2711

Oy 548 GAAATTCACAGAAATGCAACAAAAAACCAAAAAAGACAAAAACAGTCGAAA 605
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Db 2712 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2769

RESULT 15
US-09-989-735-178
: Sequence 178, Application US/09989735
: Publication No. US20020193299A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavini, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2730PIC61
: CURRENT APPLICATION NUMBER: US/09/989,735
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
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71	PRIOR APPLICATION NUMBER: 60/091626
72	PRIOR FILING DATE: 1998-07-02
73	PRIOR APPLICATION NUMBER: 60/091633
74	PRIOR FILING DATE: 1998-07-02

Thu Mar 6 08:14:02 2003

us-09-993-420a-1.rnpb

; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match	0.88;	Score 51.6;	DB 9;	Length 2773;
Best Local Similarity	55.6%;	Pred. No. 0.72;		
Matches 99;	Conservative	0;	Mismatches 79;	Indels 0;
				Gaps 0

[illegible]

Search completed: February 28, 2003, 10:05:45
Job time : 1163.42 secs


```

Db 360 AHBBAKMDVWVSHAMKWHANAHSRKKWBYKRTVNNNNNGTTMMKRMWYKMDM 419
Oy 2487 TATTTTAAAGCATATTTCTTCTGATTTGATTTGCGAAAAAGATGCTGATTTATCA 2546
Db 420 DMBGTYNNNNNGGRIYYGTTKMKMYTYKMKANCKWPAHDHKTCTHNNNTTMMKTYW 479
Oy 2547 AATCGGTTTTTAATGTAATAATTTTGGAATAATCATTTAAATTCGATTTTGAACTT 2606
Db 480 NNCYKSMNTNGKSHREAAVYTWMMWRRAHANNNNNDYMKACTYKBYVCSKMMN 539
Oy 2607 TTTCTCGAAAAACAGTTTCTGCTGATTTGCTGAAGCAAAAAACCCCAAAATTCAT 2666
Db 540 YAAWYTKSSNNTSRYYKTKNNNSMRSDTBSMGANNTYARABHYGYWNTBMMWSHT 599
Oy 2667 TTTGACATTTAAACACGAAAAATCGTTTTTAAAGCTTAATTTCCGACGAATGA 2726
Db 600 WBBBBAAGAAHYMMBYBAKCHCMKAMYKAKYAGAGGNNNNNNNNNNNNNNNNATCAR 659
Oy 2727 ACGAATTAATTCGAATTTCTATTTTCAGATAGTGTCTAATCTGCTGGCGTTTGT 2786
Db 660 DDYTAASRWYAMAANAAMWYKBAANNAVYTHANNMGCNNNAATDRRTMKNNNNNAGT 719
Oy 2787 AGCTGCAAAAATGATGGAATCCCTGGAAGTCAAGGACAGTGCAGAACCTCTGTTA 2846
Db 720 WKNNNNNNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAK 779
Oy 2847 CACATGCTGTTCATCAAAACCGGATCCGCAACAACTGGAAGAACACATTCGAGCTG 2906
Db 780 YTTNNNNNTYRGVYNTAAADGWAANNNNNNNNNNNNNNNNNSDMMVYAWANGTNNNN 839
Oy 2907 GGAAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2966
Db 840 NNNNNNAVAMTNNWYTTDDRMBAATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 899
Oy 2967 CTTCGCCGGGTGTGTAACCCGATATATACAGGGTTCGTAAGCTCTGGGGGACAG 3026
Db 900 ATKNNNAATYNNRGATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 959
Oy 3027 TCGAACAATTCATGATTTACTGTTTATGTAATGTTATGTTACGGAATACAAA 3086
Db 960 TKGWMMNCT-TTCRKYNNCTWTWMTTTRTYAATRMKTNNATGSMTRCATGKNNN 1018
Oy 3087 TTGCAACAATTCATGATTTACTGTTTATGTAATGTTATGTTACGGAATACAAA 3146
Db 1019 YWIGWKTWTAATYKATYKATYKATYKATYKATYKATYKATYKATYKATYKATYK 1078
Oy 3147 AGTAATTCCTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3204
Db 1079 GKATCYMDNAAWPTACATSMWATHKYNNHCKCNNNNNNNNNNNNNNNNNNNNNN 1136

RESULT 2
US-09-806-708B-22/c
: Sequence 22, Application US/09806708B
: GENERAL INFORMATION:
: APPLICANT: The University of British Columbia
: TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
: FILE REFERENCE: 4810-58741
: CURRENT APPLICATION NUMBER: US/09/806,708B
: PRIOR FILING DATE: 2001-04-03
: PRIOR FILING DATE: 1999-08-04
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 22
: LENGTH: 1141
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: NAME/KEY: Promoter
: LOCATION: (1)..(1141)
: OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

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Query Match 1.0%; Score 66; DB 5; Length 1141;
Best Local Similarity 13.2%; Pred. No. 0.0018;
Matches 122; Conservative 332; Mismatches 461; Indels 12; Gaps 3;

Oy 2216 ATGCACGTTTGTGAAGGAGAGAAAATAGTGAATAAAAGTTTGCAGAAAATTCG 2275
Db 1003 ATNNAAWYATTTAAVAAAKWABWAGNNMMRYGAAGNKKWCAAAATYBWBADTAGK 944
Oy 2276 CAGAAAGTGGCAGAAAACATTTGCA---AAATGTTTCTTCCCTCAGAAATC 2331
Db 943 CNNNNNNMTDVRMAKAKNNNNNNNAVYACINRAATNNKMAITHMKYTHGASHRRR 884
Oy 2332 AGCAAAATCTGTCGCAAAAATAGCCCAATATGTGCTTTTGAAGTTTCCATTAAA 2391
Db 883 HHHTCRRTKYNNNNNNNAATYVYHNAARRMNAWRTNNNNNNNNNNNNNNNNNNNN 824
Oy 2392 AACAAGATTTGATGCCGAGTTGTAATTTTGTGTAATAATAGAGAAATTT 2451
Db 823 WKHSWCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 764
Oy 2452 ACGAATTCGATTAAGATGATTTTCTAATGCAATATTTTAAAGCATATTTCTTGA 2511
Db 763 HTDWCTKWNTWTWDMATTTBTNTTNNMTSTMTNNNNNNNNNNNNNNNNNNNNNNNN 704
Oy 2512 TTTGATTTTGGAAAAAGATCTGCTGATTTATCAAAAATCGTTTTTAATGTAATTT 2571
Db 703 HATNNWGCWNNNTDARNTNTTVMRBMMNTKTRWYSTERHHYTATNNNNNNNNNN 644
Oy 2572 GTGA-----AAATACATTAATTCGATTTTGAAGTTTCTGCAAAAACAGTT 2625
Db 643 NNNNNSCCTGRMNTYRTMKDGTATYKKYKMDJTCTYDVADSWYVYAWMMCRD 584
Oy 2626 TTTCTGATTTGCTGCAAGCAAAAACCCCAAAATTCATTTTGAACATTTAAACCA 2685
Db 583 YTTTNNNTYCKSAISYVYNNNNMMWRYSARWSSARVTTNNNNMMGSBVBRWAGT 524
Oy 2686 GAAAAATGTTTTTTTAAGCTTAATTTTCCGCGCAAAATGAACATTAATTTGCAAT 2745
Db 523 MMWRHNNNNNTDTRYWMMKRWABRTTYVDSMCAKSMRGGNNWRARWMAANNDDGA 464
Oy 2746 TCTAATTTTCAATAGCTATCTGCTGCGGTTTCTGAGTCCAAAAATGATGGA 2805
Db 463 MDHWYTWGNNNTMMRRAKMMNNMWRCAATCCNNNNNNNNNNNNNNNNNNNNNNNN 404
Oy 2806 TCCGTAAGTCAAGGACCAAGTCCGAAACCTCTGTTACACATCCCTGTATCA 2865
Db 403 CNNNNBKAYMVAWMMYSDTNTDMMWNTSDWBHWYTYDYTMRAANNNNNNNNNN 344
Oy 2866 ACGCGATCCGCAACACTGGAAGACACATTCGAGCTGGTGAAGAGTATTCAT 2925
Db 343 KTTSMWMMNDHNTHTCTYGNNTWGSAYBMAAASMAAGASNBVTYNWCRWTKYK 284
Oy 2926 GACATTAGAAGCAATATCCCTTCCCTAGTACCTTGAATCCCGGGGTGTTGA 2985
Db 283 NNNNNKATYRTKYKTVAMCNRKRYDYDAWTVBKRNKYCAAYBYWBYMKHMBMRA 224
Oy 2986 GCGGATAATTAACAGGGTGTGAGCTCTTGGGGGACAGCTGGAACATATTCAGAT 3045
Db 223 BHSNNMMWVCKRKYVSMHYHAMRYKBABAVG--CNNNNKDBMAHHNNWATNNMMW 166
Oy 3046 ATTACGTTTATGATATGTTATTTGTTAGGGAATTAACAATTCAGAAATCTTTCA 3105
Db 165 WMYAYMMHHHKKKGAWTKKATBDDBAHYKTYWYKTYDWCAMCWNNAKAKRYTAMK 106
Oy 3106 CAACATATTTGACGCGCAAAATATCA 3132
Db 105 HMWYTTDRYVSAANTGVRRMMRMWCMW 79

RESULT 3
US-10-311-455-1955
: Sequence 1955, Application US/10311455

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Query March	1.0%;	Score 65.8;	DB 6;	Length 8592;
Best Local Similarity	51.9%;	Pred. No. 0.0026;		
Matches 148; Conservative	0;	Mismatches 137;	Indels 0;	Gaps 0

RESULT 4
US-10-311-455-1027

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; ORGANISM: Artificial Sequence
; FEATURE:

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Query Match	0.98;	Score 59.8;	DB 6;	Length 6294;
Best Local Similarity	47.78;	Pred. No. 0.035;		
Matches 175; Conservative	0;	Mismatches 192;	Indels 0;	Gaps 0

RESULT 5
US-10-311-455-1763/c
; Sequence 1763, Application US/10311455
: GENERAL INFORMATION

Query Match	0.9%	Score 56;	DB 6;	Length 5324;
Best Local Similarity	49.4%	Pred. No. 0.19;		
Matches 235; Conservative	0;	Mismatches 230;	Indels 11;	Gaps 3

2532 AGCCCAATATGTCCTTTTGAAGTTTCCATTAAAAACACGAACTTGTGATCCG 2411

Db 1039 AAAAAATTAATTAATTTTAAACCAATTTTAAATTAACACG--TTAACTTCA 983
OY 2412 GATTCGAAATTTTGGTGAATTAATTTAGCAGAAATTTAGCAATTTAAACGTT 2471
Db 982 TTTTTCCTAATTCACATTAATTTATTCATTTAAATTTAAATAATTAATCTTCT 923
OY 2472 TATTTTCATTCGAAATTTTAAACCAATTTTCTGATTTGATTTGGCAAAACAT 2531
Db 922 TATATATTTAAATTAATTTTAAACCAATTTATTCATTTAAATTTAAATAATTC 863
OY 2532 CTGCTGATTTTCAAAAATCGTTTAAATTTAAATTTGGAATTAATTAATTT 2591
Db 862 CAACATTTTAAATTAATTAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 808
OY 2592 CGATTTTGAATTTTCTGCAAAACAGTTTCTGCTGATTTGCTGAACGAAATA 2651
Db 807 ATATTTATTAATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 748
OY 2652 CCCCCAAATTCATTTTGCACATTTAAACCAAGAAATCGTTTAAAGCTTAAT 2711
Db 747 CATTAAAT--AATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 691
OY 2712 TTCCGCCAGAAATGAAGATTTAAATTTCAATTTTCAATTTGATAGTCTAA 2767
Db 690 TTATTTCTATTAATTAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 635

RESULT 6
US-10-311-455-426
Sequence 426, Application US/10311455

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311.455
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 426
LENGTH: 6980
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-426

Query Match 0.8%; Score 55.6; DB 6; Length 6980;
Best Local Similarity 49.0%; Pred. No. 0.23;
Matches 148; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

OY 2401 TTTTATCCCGATGTAATTTTGTGATTAATTTAGCAGAAATTTAGCAATTCG 2460
Db 3415 TTTTATGATGATGAGAAATTTTATGTTGATTAATTTTAAATTTAGCTTTATTTT 3474
OY 2461 ATTTAAAGCTATTTTCATTCGAAATTTTAAAGCAATTTTCTGATTTGATTT 2520
Db 3475 TTTTATTAATTTTGTGTTATGATTAATTTAAATTTATTTTCTGATTTATG 3534
OY 2521 CGGAAAAACATCTGCTGATTTTCAAAAATCGTTTAAATTTGTAATTTTGTGAAAT 2580
Db 3535 TTTTATGATGATGAGAAATTTTAAAGCAATTTTAAAGCAATTTTAAATTTAA 3594
OY 2581 ACATTAATTTGATTTTGAATTTTCTGCAAAACAGTTTCTGCTGATTTGC 2640
Db 3595 GTTTTGAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 3654

OY 2641 TGAACGAAATCCCAAAATTCATTTTGCATTTAAACCAAGAAATCGTTT 2700
Db 3655 TAAAGATTAATTTTAAAGGATTTTATTTTATTTTATTTTATTTTATTTTATTT 3714
OY 2701 TA 2702
Db 3715 TA 3716

RESULT 7
US-10-312-841-2
Sequence 2, Application US/10312841

GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des menschlichen Genoms
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312.841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
NAME/KEY: unsure
LOCATION: (379615)
US-10-312-841-2

Query Match 0.8%; Score 55.6; DB 6; Length 3673778;
Best Local Similarity 47.9%; Pred. No. 0.56; Indels 0; Gaps 0;
Matches 160; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

OY 2413 ATTTGATTTTGTGATTAATTTAGCAGAAATTTAGCAATTTGATTAATTTAG 2472
Db 929075 ATTTTGTATTAATTTATGATGATTAATTTAAATTTAGGCGCAAAAGAAATAT 929134
OY 2473 ATTTTGTATTAATTTATGATGATTAATTTAAAGCAATTTTCTGATTTGATTT 2532
Db 929135 TTTTATTTATTTAGATTAATTTAAAGCAATTTGATTAATTTAAAGCAATTTAT 929194
OY 2533 TGTGATTTATCAAAATTCGTTTAAATTTGTAATTTGTAATTTGTAATTTGTA 2592
Db 929195 TATGATTTATGATTAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTA 2592
OY 2593 GATTTTGAATTTTCTGCAAAACAGTTTCTGCTGATTTGCTGAACGAAATTC 2652
Db 929255 AATGATGATGAGGAGGAGGAAATTTATTAATTTGATTTATTAATTTAAGATTA 929314
OY 2653 CCCCCAAATTTCAATTTTGCACATTTAAACCAAGAAATCGTTTAAAGCTTAATTT 2712
Db 929315 TATATGATTTAAATTTAAATTTGAAATTTGAAATTTGAAATTTGAAATTTG 929374
OY 2713 TCCGCCAGAAATGAAGATTTAAATTTGCAAAATTT 2746
Db 929375 GTCTGATTTAAATTTAAATTTTAAATTT 929408

RESULT 8
US-10-311-455-1102
Sequence 1102, Application US/10311455

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311.455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537

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; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1102
; LENGTH: 9204
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1102

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Query Match
Best Local Similarity 47.6%; DB 6; Length 9204;
Matches 160; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

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QY 2308 TTGTTGTTTCTCAGGAAATCAGCAAACTGTCAGAAATAGCCCAATTAATGTC 2367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5110 TTTTATTTTATTTTAAAGATATTTTAAATAGTATGATATGTTATTTT 5169
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2368 TTTTGAAGTTTCCATTAATAAACAAGATTTGATCCGATGTAATTTT 2427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5170 TTTTAAATGTTGGTATTAATGTTATTTGATTTGTTTATTTTAAATTTGA 5229
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2428 GTTGAAATTTAGCAAAACTTACGAATTCGATTAATAAGTTATTTCTATTCGAAT 2487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5230 TTTATTTATTTAGATTAAGTTTATTTGTTTATGTTGTTGTTTAAATGTTGAT 5289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2488 ATTTTAAAGCATTTTCTGATTTGTTTATTTGGAATAAGATCTGCTATTAACAA 2547
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5290 TATTTATTTTATTTTATTTTATTTTAAAGTTGATTAAGATTAAGATTAAGATTTG 5349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2548 AATCGTTTATTAATGTAATAATTTGGAATAATTCATTAATAATTTTGAATTT 2607
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5350 TTTAGTTTATTTTATTAATTAATTAATGATGAGATTCGTTTATTAATTTTAAAGTTT 5409
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2608 TTCTCGAAAAAAGAGTTTCTGCTGATTTGCTGA 2663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5410 ATTTTATTTTATTTATTTATTTATTTATTTATTTA 5445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 9
US-10-311-455-1474/c
; Sequence 1474, Application US/10311455
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1474
; LENGTH: 9157
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1474

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Query Match
Best Local Similarity 45.1%; DB 6; Length 9157;
Matches 290; Conservative 0; Mismatches 347; Indels 6; Gaps 3;

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QY 4829 TTTTATAGAAAAATGATTTTATTTATTCAAAAATTTATTTACGATCGCAAAA 4888
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2717 TTTTATAGAAAAATGATTTTATTTATTTAAAAATTTATTTATTTCAATACATAAAA 2658
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4889 CAAATGAGACACCGATTAATAATTCGACCAACAAATAGTTGAATTTAGTACT 4948
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2657 CTAACATTAATCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2598
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4949 TTTAAGGNGNCATTTCTATTTTTCACACAACTGTGTGTGNNNGGATATCG 5008
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2597 TCTCTACCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2538
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5009 TCATTTTGTAGAGAAATCAAGA--AAATGCAATATATGTTCAAAAAAACCACATTAATG 5066
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2537 TCTTTAAAAAACCATAATTTCTATTAATTAATTAATTAATTAATTAATTAATTAATTA 2478
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5067 CGAATTTCAAGCTTGAAACGAAATTCAGAAATTTCTAAATTTAAAAAATCATTTG 5126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2477 AAAAAAATAAATAATTTCTTTTACACCATTAATTAATTAATTAATTAATTAATTAATTA 2419
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5127 AATGTAATTTGATTAATTTCACTTGAAGTCATATGCAATTTGCTATTTCCGNNNT 5186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2418 ATTTCAAAATTAATTTCTTTTACATTAATTAATTAATTAATTAATTAATTAATTAATTA 2359
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5187 TCGAATTTTGTCTCAGCTGCGCGGAGAAAGAGAACGAGNNAATGATTTCTGCA 5246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2358 AAAAAAATAATTTCTCACCACCATTAATTAATTAATTAATTAATTAATTAATTAATTA 2299
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5247 TTTTCTGTCGTCGTCATTAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 5306
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2298 ATTTTACATTAATTAATTAATTTTCCATTAATTAATTTTAAATTTTAAATTTTAAATTT 2239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5307 GACAATTTGATTAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCA 5366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2238 AACAATTA--ACCATTAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCA 2182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5367 AAAAAAAGCAAAACCTCTAGCTTTAGCTTGCAATTAATTTGCAATTTGCAATTTGCA 5426
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2181 AAAAAAATAAATAATTTTCAACCTTAATTAATTAATTAATTAATTAATTTTAAATTTTAA 2122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5427 AAAAACTTAATTTCTGCAACCTTACAGCTTAATTAATTTGCAATTTGCAATTTGCA 5469
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2121 ATATTTCTTAATAACATTAATTAATTAATTAATTAATTAATTTTAAATTTTAA 2079
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 10
US-10-311-455-1721
; Sequence 1721, Application US/10311455
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1721
; LENGTH: 11805
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1721

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[illegible]

Query Match	0.8%	Score 53.6	DB 6	Length 14987	
Best Local Similarity	50.0%	Pred. No. 0.63			
Matches 134	Conservative	0	Mismatches 134	Indels 0	Gaps 0
OY 2370	TTTTGAAGCTTTCCATTAATAAACACGCAATTTTGATCCCGGATGTAAATTTTTTTCG				2429
Db 12448	TTTTTAAAGTAATTAATTTAGATAAATATGACCTTTTATTTTACGTTTAAATAGTATT				12507
OY 2430	TGATAATTGGCAAAACCTTTCGCAATTCGATTTAAACCTTTATTTTCATTCGAAAT				2489
OY 12508	TAAATAGTAATAGAAAAGTTTGATTTTATATAGAAAGTATATGACTTTTAAAGTAGT				12567
OY 2490	TTTTAAAGCATATTTTCCTTGATTTGTATTTTCGCAAAAAGATCTCGATTTATCAAAA				2549
Db 12568	TTTTTAATTAATTTAAATTTAATTAATAAAGTGTATTAATGATCGCTTATATTTTAAAAA				12627
OY 2550	TCGGTTTTAAATCTAAATTTTTCGAAAATACATTTAAATTCGATTTTTCGACTTTT				2609

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 18:42:50 ; Search time 7944.47 Seconds

(without alignments)

13373.121 Million cell updates/sec

Title: US-09-993-420A-1

Perfect score: 6560

Sequence: 1 atcgatagtcgtcaccaaat.....gtttgtataaaattctcaa 6560

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched:

16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:

32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estlin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estrom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_hiv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	554	8.4	672	9	AU214778
C 2	544	8.3	640	9	AU216828
C 3	533.4	8.1	706	13	BJ135657
C 4	529	8.1	593	13	BJ124068
C 5	514.8	7.8	638	13	BJ143512
C 6	513	7.8	587	13	BJ152426

C 7	473.4	7.2	556	9	AU215190	AU215190
C 8	470.8	7.2	562	13	BJ134935	BJ134935
C 9	433.4	6.6	606	13	BJ107235	BJ107235
C 10	365.4	5.6	515	9	AU203561	AU203561
C 11	324.6	4.9	502	13	BJ103911	BJ103911
C 12	323	4.9	501	9	AU202666	AU202666
C 13	323	4.9	502	13	BJ114579	BJ114579
C 14	322.4	4.9	500	13	BJ101104	BJ101104
C 15	318	4.8	360	9	AV190122	AV190122
C 16	314.6	4.8	323	14	D73048	D73048
C 17	312.4	4.8	372	9	AV186746	AV186746
C 18	311.4	4.7	676	13	BJ149838	BJ149838
C 19	308	4.7	377	14	C47713	C47713
C 20	307.2	4.7	488	9	AU214274	AU214274
C 21	304	4.6	377	9	AV191091	AV191091
C 22	303.4	4.6	709	13	BJ143970	BJ143970
C 23	303	4.6	377	14	C49742	C49742
C 24	302	4.6	360	14	C39347	C39347
C 25	301	4.6	376	9	AV192163	AV192163
C 26	300	4.6	375	9	AV195166	AV195166
C 27	299	4.6	300	9	AV181369	AV181369
C 28	297	4.5	375	14	C42506	C42506
C 29	295.8	4.5	360	9	AV192562	AV192562
C 30	285.4	4.4	360	9	AV201872	AV201872
C 31	279.6	4.3	300	14	C39078	C39078
C 32	275.6	4.2	300	14	C31912	C31912
C 33	274	4.2	482	13	BJ131523	BJ131523
C 34	273.2	4.2	307	14	M79968	M79968
C 35	269.8	4.1	300	9	AV113305	AV113305
C 36	269.2	4.1	300	14	C29364	C29364
C 37	268.2	4.1	300	9	AV112965	AV112965
C 38	267.2	4.1	300	9	AV199224	AV199224
C 39	265	4.0	300	14	C59958	C59958
C 40	265	4.0	300	9	AV114599	AV114599
C 41	259.4	4.0	300	9	AV179317	AV179317
C 42	256	3.9	300	9	AV114409	AV114409
C 43	254.6	3.9	300	9	AV114279	AV114279
C 44	250.4	3.8	510	3	AU218099	AU218099
C 45	247.8	3.8	300	9	AU116690	AU116690

ALIGNMENTS

RESULT 1
AU214778/c 672 bp mRNA linear EST 17-Jul-2001
DEFINITION AU214778 unpublished oligo-capped cDNA library, stage 12
LOCUS AU214778
VERSION AU214778
KEYWORDS
SOURCE
ORGANISM
EST.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Pelodierinae; Caenorhabditis.
1 (bases 1 to 672)
Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
A complementary view of the C.elegans genome
Unpublished (2001)
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"

FEATURES

source

/clone_lib="yk817c09"
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/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pC86"

BASE COUNT 212 a 128 c 183 g 147 t 2 others

ORIGIN

Query Match 8.4%; Score 554; DB 9; Length 672;
Best Local Similarity 91.2%; Pred. No. 3.7e-78;
Matches 620; Conservative 0; Mismatches 7; Indels 53; Gaps 1;

968 AGTCGAGGCAAGACGCAATCCAGAAATTCGATGGAATACCTGTGAGGAGGCT 1027
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630 AGTCGAGGCAAGACGCAATCCAGAAATTCGATGGAATACCTGTGAGGAGGCT 571
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1028 CCAAGAAATCGCCCAATGCTCCACATCTCAGGCTACAGCCCAATTTGACTGATGC 1087
|||||
570 CCAAGAAATCGCCCAATGCTCCACATCTCAGGCTACAGCCCAATTTGACTGATGC 511
|||||
1088 TCTCCGATTCATGAAATCAGCGGTTGTATGCGCGGAAACCTTCTCGGAGGAA 1147
|||||
510 TCTCCGATTCATGAAATCAGCGGTTGTATGCGCGGAAACCTTCTCGGAGGAA 451
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1148 TCGGATTCGCAATTTTCCGCTTCGATTCACCGCTTTTGGATTTCAATCGTACCTGA 1207
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450 TCGGATTCGCAATTTTCCGCTTCGATTCACCGCTTTTGGATTTCAATCGTACCTGA 391
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1208 ACTTACCATGCGCGGAGACCGCTGCTTCAAGTACATCATTTCCCATCATTTTC 1267
|||||
390 ACTTACCATGCGCGGAGACCGCTGCTTCAAGTACATCATTTCCCATCATTTTC 331
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1268 ATACTCTTAAGCAATTCGCTTCTTGAATTCGATTTGGCTAAGGAGCATTAATGTTG 1327
|||||
330 ATACTCTTAAGCAATTCGCTTCTTGAATTCGATTTGGCTAAGGAGCATTAATGTTG 271
|||||
1328 GACAGGTAGAGTTGAATTAATTAATTTTAAATAAATTAATTTTCAGAT 1387
|||||
270 GA-----CAGAT 264
|||||
1388 CTACAAATCGGGAATCTCGTATCTGAGACTTTGGCTATTTCTGCTCGCAATTTGCT 1447
|||||
263 CTACAAATCGGGAATCTCGTATCTGAGACTTTGGCTATTTCTGCTCGCAATTTGCT 204
|||||
1448 CAACCTCTGGCAGAAAGAGCAAGAACTGCTAGGACAGATGCTCGGCTTTCT 1507
|||||
203 CAACCTCTGGCAGAAAGAGCAAGAACTGCTAGGACAGATGCTCGGCTTTCT 144
|||||
1508 TTCTTACTCGCCGCAACCTCGCAATTCGCTCAATTTACTTTACGTTATTTCT 1567
|||||
143 TTCTTACTCGCCGCAACCTCGCAATTCGCTCAATTTACTTTACGTTATTTCT 84
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1568 CGATTTCTCTTTTCCGCTAGATTTACCTGCTCTGCTTTTCTGCTGCTAGA 1627
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83 CGATTTCTCTTTTCCGCTAGATTTACCTGCTCTGCTTTTCTGCTGCTAGA 24
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1628 ATGTATATTATGATTATGAA 1647
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23 ATGTATATTATGATTATGAA 4
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RESULT 2
AU216828/c 640 bp mRNA linear EST 17-JUL-2001
LOCUS AU216828
DEFINITION Caenorhabditis elegans cDNA clone yk842e12 3', mRNA sequence.
ACCESSION AU216828

VERSION AU216828.1 GI:14854985
KEYWORDS EST
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans

REFERENCE 1 (bases 1 to 640)
AUTHORS Kohara, Y., Shinn, I. T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
COMMENT A complementary view of the C. elegans genome
Unpublished (2001)
CONTACT: Yui Kohara
Genome Biology Lab.
National Institute of Genetics
Yatai 111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES

source

1. 640
/organism="Caenorhabditis elegans"
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/db_xref="taxon:6239"
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/clone_lib="unpublished oligo-capped cDNA library, stage L4"
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/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pC86"

BASE COUNT 204 a 123 c 174 g 138 t 1 others

Query Match 8.3%; Score 544; DB 9; Length 640;
Best Local Similarity 91.8%; Pred. No. 1.4e-76;
Matches 607; Conservative 0; Mismatches 1; Indels 53; Gaps 1;

968 AGTCGAGGCAAGACGCAATCCAGAAATTCGATGGAATACCTGTGAGGAGGCT 1027
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618 AGTCGAGGCAAGACGCAATCCAGAAATTCGATGGAATACCTGTGAGGAGGCT 559
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1028 CCAAGAAATCGCCCAATGCTCCACATCTCAGGCTACAGCCCAATTTGACTGATGC 1087
|||||
558 CCAAGAAATCGCCCAATGCTCCACATCTCAGGCTACAGCCCAATTTGACTGATGC 499
|||||
1088 TCTCCGATTCATGAAATCAGCGGTTGTATGCGCGGAAACCTTCTCGGAGGAA 1147
|||||
498 TCTCCGATTCATGAAATCAGCGGTTGTATGCGCGGAAACCTTCTCGGAGGAA 439
|||||
1148 TCGGATTCGCAATTTTCCGCTTCGATTCACCGCTTTTGGATTTCAATCGTACCTGA 1207
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438 TCGGATTCGCAATTTTCCGCTTCGATTCACCGCTTTTGGATTTCAATCGTACCTGA 379
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1208 ACTTACCATGCGCGGAGACCGCTGCTTCAAGTACATCATTTCCCATCATTTTC 1267
|||||
378 ACTTACCATGCGCGGAGACCGCTGCTTCAAGTACATCATTTCCCATCATTTTC 319
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1268 ATACTCTTAAGCAATTCGCTTCTTGAATTCGATTTGGCTAAGGAGCATTAATGTTG 1327
|||||
318 ATACTCTTAAGCAATTCGCTTCTTGAATTCGATTTGGCTAAGGAGCATTAATGTTG 259
|||||
1328 GACAGGTAGAGTTGAATTAATTAATTTTAAATAAATTAATTTTCAGAT 1387
|||||
258 GA-----CAGAT 252
|||||
1388 CTACAAATCGGGAATCTCGTATCTGAGACTTTGGCTATTTCTGCTCGCAATTTGCT 1447
|||||
251 CTACAAATCGGGAATCTCGTATCTGAGACTTTGGCTATTTCTGCTCGCAATTTGCT 192
|||||

Qy	1448	CAACCTTTGGCCAGAAACAAGACCAACAAGACTGCTTAAAGGCACGATGCTCCGCCTTCTTTT	1507
Db	191	CACCTCTTGGCCAGAAACAAGACCAACAAGACTGCTTAAAGGCACGATGCTCCGCCTTCTTTT	132
Qy	1508	TTTCTTACTCGCCCGACGCCCTCGACAATTCTGTCAATTTACTTTTACCGTTGATTTCTT	1567
Db	131	TTTCTTACTCGCCCGACGCCCTCGACAATTCTGTCAATTTTACTTTTACCGTTGATTTCTT	72
Qy	1568	CGATTTTCTCTCTTTTCCGATATTTACCTCTCTCTCGTTTTTTTTTCTCTCTCTAGA	1627
Db	71	CGATTTTCTCTCTTTTCCGATATTTTAACTCTCTCTCTGTTTTTTTTTCTCTCTCTAGN	12
Qy	1628	A	
Db	11	A	11

RESULT 3	BJ135657/c	706 bp	MRNA	EST 23-JAN-2002
LOCUS	BJ135657/c			
DEFINITION	BJ135657	unpublished o1190-capped cDNA library, C. elegans L1 stages		
ACCESSION	Caenorhabditis elegans cDNA library, C. elegans L1 stages			
VERSION	BJ135657			
KEYWORDS	BJ135657.1	GI:18295814		
SOURCE	EST.			
ORGANISM	Caenorhabditis elegans.			
	Caenorhabditis elegans.			
	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea			
REFERENCE	; Rhabditidae; Peloderinae; Caenorhabditis.			
AUTHORS	1 (bases 1 to 706)			
	Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.			
	and Suganum, S.			
TITLE	A complementary view of the C. elegans genome			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Tadasu Shin-1			

FEATURES	LIBRARY
source	csunniyenes.nlg.ac.jp
	Location/Qualifiers
	1. .706

BASE COUNT	222 a	140 c	194 g	148 t	2 others
ORIGIN					

Query Match	8.13;	Score 533.4;	DB 13;	Length 706;
Best Local Similarity	91.6%;	Prod. No. 6.5e-75;		
Matches 597;	Conservative	0;	Mismatches 2;	Indels 53;
				Gaps 1

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Db	599	AGTCCGAGGCAAGAGCCCAATCCAGAAAGTTGGATGGGAAATCACTGTTGAAGCAGCGT	540
QY	1028	CCAAGAATCGCCCATATGCTCCACATCTCAACGTTCAACAGCCACAAATTAACCTGGATGC	1087
Db	539	CCAAGAATCGCCCATATGCTCCACATCTCAACGTTCAACAGCCACAAATTAACCTGGATGC	480
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[illegible]

TITLE
JOURNAL
COMMENT
and Sugano, S.
A complementary view of the *C. elegans* genome
Unpublished (2002)
Contact: Tadashi Shin-i, Suzuki, Y.

FEATURES	source
Location/Qualifiers	1. .593

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/strain="N2"
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/tissue_type="whole animal"
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/notes="The AD-irrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of

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all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pCR8[®]

BASE COUNT 123 a 160 c 111 g 198 t 1 others

Query Match 8.1%; Score 529; DB 13; Length 593;
Best Local Similarity 91.6%; Pred. No. 3,5e-74;
Matches 592; Conservative 0; Mismatches 1; Indels 53; Gaps 1;

999 CGGATGGGAATACCTGTTGAAGCAGCGCTCCAGAAATCGCCCAATGCTTCACATCTCAC 1058
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1 CGGATGGGAATACCTGTTGAAGCAGCGCTCCAGAAATCGCCCAATGCTTCACATCTCAC 60
1059 CGCTACACGCCACAAATGACCTGGATGCTCCGGATTCATGAAATCAGCGTTGTGT 1118
|||||
61 CGCTACACGCCACAAATGACCTGGATGCTCCGGATTCATGAAATCAGCGTTGTGT 120
1119 AATGGCCGGAACCTTCCTGCGAGAGAAATCGAATTCGCAATTTGCCGTTGCATTTTAC 1178
|||||
121 AATGGCCGGAACCTTCCTGCGAGAGAAATCGAATTCGCAATTTGCCGTTGCATTTTAC 180
1179 CGCTTTTGATTTTCATCCGAGTCTGCACTTACATGCGCGGTGACCGCTGCTTCAA 1238
181 CGCTTTTGATTTTCATCCGAGTCTGCACTTACATGCGCGGTGACCGCTGCTTCAA 240
1239 GTACATCATGCTTCCCATCATCTTTCATACGGAATTCGCTTTAGAGATT 1298
|||||
241 GTACATCATGCTTCCCATCATCTTTCATACGGAATTCGCTTTAGAGATT 300
1299 CGATTTGGCTAAGGAGTCAATATGTTGACAGTAGAGATTGAATTTAATTTAAT 1358
301 CGATTTGGCTAAGGAGTCAATATGTTGACAGTAGAGATTGAATTTAATTTAAT 331
1359 TGTTTTAAATTAATTTTTCAGATCTTCAATCGGATATCTGTATCTGACTT 1418
332 -----CAGATCTTCAATCGGATATCTGTATCTGACTT 367
1419 TCGGCTATTTCTGCTTCGCATTTGTTCAACTCTTCCCAACAAAGCAAGCAAGACT 1478
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368 TCGGCTATTTCTGCTTCGCATTTGTTCAACTCTTCCCAACAAAGCAAGCAAGACT 427
1479 GCTTAGGACAGATGCTCGCGCTTCTTTTCTTACTCGCCCAAGCCCTCGACATTTCT 1538
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428 GCTTAGGACAGATGCTCGCGCTTCTTTTCTTACTCGCCCAAGCCCTCGACATTTCT 487
1539 CGTCAATTTTACTTTCACGTTGATTTCTTCGATTTTCTCTTTTCCGTAATTTACCTTC 1598
488 CGTCAATTTTACTTTCACGTTGATTTCTTCGATTTTCTCTTTTCCGTAATTTACCTTC 547
1599 TCTCTCTGTTTTTTTTTCTCTGCTAGAAATGATATTAATGATTAAT 1644
548 TCTCTCTGTTTTTTTTTCTCTGCTAGAAATGATATTAATGATTAAT 593

RESULT 5
BU143512/c 638 bp mRNA linear EST 23-JAN-2002
LOCUS BU143512 unpublished oligo-capped cDNA library, C. elegans L1 stage
DEFINITION Caenorhabditis elegans cDNA clone YK1196h12.3', mRNA sequence.
ACCESSION BU143512
VERSION BU143512.1 GI:18303678
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabdilitoidea
; Rhabdilitidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 638)
AUTHORS Kohara, Y., Shin-1, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
TITLE A complementary view of the C. elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadashi Shin-1

Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
1. 638

FEATURES

source

/organism="Caenorhabditis elegans"
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/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pCR8[®]

BASE COUNT

203 a 124 c 164 g 132 t 15 others

Query Match 7.8%; Score 514.8; DB 13; Length 638;
Best Local Similarity 89.2%; Pred. No. 6e-72;
Matches 579; Conservative 0; Mismatches 17; Indels 53; Gaps 1;

968 AGTCCGAGGAAGAGCGCCCAATCCAGAAATGCGGAAATACCTGTTGAAGCAGCGCT 1027.
600 AGTCCGAGGAAGAGCGCCCAATCCAGAAATGCGGAAATACCTGTTGAAGCAGCGCT 541
1028 CCAAGATCCGCCCAATGCTCCATCTCACCGCTTACACGCCCAATGAGCTGGATGC 1087
540 CCAAGATCCGCCCAATGCTCCATCTCACCGCTTACACGCCCAATGAGCTGGATGC 481
1088 TCTCCGATTCATAGAAATGAGCGGTTGTGAATGGCCGGAACCCCTTTCGAGAGAA 1147
480 TCTCCGATTCATAGAAATGAGCGGTTGTGAATGGCCGGAACCCCTTTCGAGAGAA 421
1148 TCGATTCGCGAGTTTTCGCTTTCATTTCAACCGCTTTTGGATTTTATCCGTAAGCTGGA 1207
420 TCGATTCGCGAGTTTTCGCTTTCATTTCAACCGCTTTTGGATTTTATCCGTAAGCTGGA 361
1208 ACTTACCATGCGCGGTGACCGCTGTTTCAAGTACATCATTTGCTTCCCATTTTCC 1267
360 ACTTACCATGCGCGGTGACCGCTGTTTCAAGTACATCATTTGCTTCCCATTTTCC 301
1268 ATACTCTTAACGGAATTCGCTTTCAGATTTGATTTGCTTAAGGAGTCAATATGTTG 1327
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240 GA-----CAGAT 234
1388 CTACAAATCGGATATTCGATCTGACTTTCGCTATTTCTGCTTCGCAATTTGCTT 1447
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1448 CAACCTTTCGCGAGAACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 1507
173 CAACCTTTCGCGAGAACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 114
1508 TTCTTACCTCGCCCGAGCCCTGACATTTCTGCTAATTTTACTTTTACCGTTGATTTCTT 1567
113 TTCTTACCTCGCCCGAGCCCTGACATTTCTGCTAATTTTACTTTTACCGTTGATTTCTT 54
1568 CGATTTTCTCTTTTTCGTAATTTTACCTTCTCTCTTTTCTTTTCTTTTCTTTTCTTT 1616
53 CGATTTTCTCTTTTTCGTAATTTTACCTTCTCTCTTTTCTTTTCTTTTCTTTTCTTT 5

RESULT 6
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 LOCUS BUI52426 unpublished oligo-capped cDNA library, C. elegans L1 stage
 DEFINITION Caenorhabditis elegans cDNA clone yk1307b04 3', mRNA sequence.
 ACCESSION BUI52426
 VERSION BUI52426.1 GI:18320411
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
 ; Rhabditidae; Pelodierinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 587)
 Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
 and Sugano, S.
 A complementary view of the C. elegans genome
 Unpublished (2002)
 CONTACT: Tadashi Shin-I
 CENTER: National Institute of Genetics
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genetics.nig.ac.jp.
 FEATURES
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 elegans L1 stage"
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 /dev_stage="L1"
 /note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"
 BASE COUNT 194 a 111 c 160 g 121 t 1 others
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 Best Local Similarity 91.4%; Pred. No. 1.2e-71;
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 QY 999 CGGATGGGAATACCTGTTGAAGCAGCGCTCCAGAAATCGCCCAATCGCTCCACATCTCAC 1058
 DB 587 CGGATGGGAATACCTGTTGAAGCAGCGCTCCAGAAATCGCCCAATCGCTCCACATCTCAC 528
 QY 1059 CGTTCACAGCACAATTTGACCTGATGCTCTCGGATTCATAGAAATCAGCGGTGTGCT 1118
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 QY 1119 AATGCGCGGAACCTCTCTCGTGGAGGAATCGATTCGCGATTTGCGGTGATTTGAC 1178
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 QY 1179 CGCTTTGTGATTTACCTGCTAGCGGAATTCACATCGCGGTGACCGCTGCTTCAA 1238
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 QY 1239 GTACATCATTTGCTTTCCCATCATTTTCCATCTTAAAGGAATTCGCTTAAAGATT 1298
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 QY 1299 CGATTTGGCTAAGGAGGATCAATTAATGTTGACAGAGTAGAGATTGAATTAATTAAT 1358
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 QY 1359 TGTTTTAAATAAATAATTAATTTGAGATCTACAAATCGGATATCTGATCTGACCTT 1418

DB 256 -----CAGATCTACAAATCGGATATCTGATCTGACCTT 221
 QY 1419 TCGGCTATTTCTGCTTCGCCATTTGCTTCACATCTTGCAGAAAGAGCAACAGACT 1478
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 DB 100 CGTCAATTTACTTTTACCGTTGATTTCTTCTGATTTCTCTCTTCCGAGATTACCTC 41
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 LOCUS AU215190 unpublished oligo-capped cDNA library, stage L2
 DEFINITION Caenorhabditis elegans cDNA clone yk822e10 3', mRNA sequence.
 ACCESSION AU215190
 VERSION AU215190.1 GI:14853347
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
 ; Rhabditidae; Pelodierinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 556)
 Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
 and Sugano, S.
 A complementary view of the C. elegans genome
 Unpublished (2001)
 CONTACT: Yuji Kohara
 CENTER: National Institute of Genetics
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykoha@genetics.nig.ac.jp.
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 /note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"
 BASE COUNT 157 a 114 c 158 g 127 t
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 QY 1028 CCAAGATCGCCCAATTCGATTCACATCTCAGCGGTTCACAGCCCAATTCGATTCG 1087

BASE COUNT	187 a	103 c	155 g	114 t	3 others
ORIGIN	subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pC86*				
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Best Local Similarity	90.2%; Pred. No. 5, 8e-65;				
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OY 1025	GCTCCAGAAATCGCCCAATGCTTCACATCTCATCGCTACACGCCACCAATGAGCTGGA 1084				
DB 562	GCTCCAGAAATCGCCCAATGCTTCACATCTCATCGCTACACGCCACCAATGAGCTGGA 503				
OY 1085	TGCTTCGCGGAAATTCATAGATCAGCGGTGTGTAAATGGCCGGAAACCTTCTCTGGAG 1144				
DB 502	TGCTTCGCGGAAATTCATAGATCAGCGGTGTGTAAATGGCCGGAAACCTTCTCTGGAG 443				
OY 1145	GAATCGGATTCGCACTTTTGGCCGTTCCATTTCACCGGTTTGTGGATTCATCCGTAAGT 1204				
DB 442	GAATCGGATTCGCACTTTTGGCCGTTCCATTTCACCGGTTTGTGGATTCATCCGTAAGT 383				
OY 1205	GGAACTTACCATCGCGGTGACCGGTGTCTTCAAGTACATCATTTGCTTCCCATATT 1264				
DB 382	GGAACTTACCATCGCGGTGACCGGTGTCTTCAAGTACATCATTTGCTTCCCATATT 323				
OY 1265	TCCATACCTCTTAAGGAATTCGCTTCTTAGATTCGATTTGGCTTAAGGAGTCAATATG 1324				
DB 322	TCCATACCTCTTAAGGAATTCGCTTCTTAGATTCGATTTGGCTTAAGGAGTCAATATG 263				
OY 1325	TTGGACACGGTAGGAGTTCATTAATTATTAATTTATTTTAAAAATAAATTTCA 1384				
DB 262	TTGGACACGGTAGGAGTTCATTAATTATTAATTTATTTTAAAAATAAATTTCA 256				
OY 1385	GATCTACAAATGGGATATCTGTATCTGATCTGATCTGCTATCTGCTCGGCATTGT 1444				
DB 255	GATCTACAAATGGGATATCTGTATCTGATCTGATCTGCTATCTGCTCGGCATTGT 196				
OY 1445	CTTCAACTCTTGGCACAAGACAGACAAAGACTGCTTAGGACAGATGCTCCGCTTCT 1504				
DB 195	CTTCAACTCTTGGCACAAGACAGACAAAGACTGCTTAGGACAGATGCTCCGCTTCT 136				
OY 1505	TTTTTCTTACTCGCCCGACGCCCTCGACAAATCTGTCATTTACTTTTACCGTGAATTT 1564				
DB 135	TTTTTCTTACTCGCCCGACGCCCTCGACAAATCTGTCATTTACTTTTACCGTGAATTT 76				
OY 1565	CTTGATTTTCTCTCTTTTCCGTAGATTACCTCTCTT-CTTGGTTTTTTTTTCTCTCTC 1623				
DB 75	CTTGATTTTCTCTCTTTTCCGTAGATTACCTCTCTCTCTCTCTCTCTCTCTCTCTC 16				
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DB 15	TAGAA 11				
REFSEQ 9	606 bp mRNA linear EST 23-JAN-2002				
BI107235	BI107235 unpublished oligo-capped cDNA library, C. elegans L1 stage				
LOCUS	BI107235 unpublished oligo-capped cDNA library, C. elegans L1 stage				
DEFINITION	Caenorhabditis elegans cDNA clone yk1094c02 5', mRNA sequence.				
ACCESSION	BI107235				
VERSION	BI107235.1 GI:18267260				
KEYWORDS	EST.				
SOURCE	Caenorhabditis elegans.				
ORGANISM	Caenorhabditis elegans.				
REFERENCE	Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.				
AUTHORS	Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.				
TITLE	A complementary view of the C. elegans genome				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Tadasu Shin-I				
	Center for Genetic Resource Information				

National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES
Source
Location/Qualifiers

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/tissue.type="whole animal"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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DB 169 CCAAGATGCGCCCAATCCGATCCATCTCACCCTTACAGCCCAATTCAGCTGATGC 228
QY 1088 TCTCCGATTCAGAAATCAACGCGTTGTAAATGCGGAAACCTCTCTCGCGAGAA 1147
DB 229 TCTCCGATTCAGAAATCAACGCGTTGTAAATGCGGAAACCTCTCTCGCGAGAA 288
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LOCUS AU203561
DEFINITION AU203561 unpublished oligo-capped cDNA library, stage L2

ACCESSION
AU203561
VERSION
AU203561.1 GI:14834309
KEYWORDS
EST.
SOURCE
ORGANISM
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoida
1 (bases 1 to 515)
REFERENCE
AUTHORS
Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
and Sugano, S.
TITLE
A complementary view of the C. elegans genome
JOURNAL
Unpublished (2001)
COMMENT
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers

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/dev_stage="L2"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
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DB 482 GACAGGT 488
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RESULT 11

RESULT 14					
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LOCUS					
DEFINITION	BT101104	unpublished oligo-capped	CDNA library,	C. elegans	L1 stage

Accession	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment	Features
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Bj101104										
Bj101104.1	GI:18243774									
EST										
Caenorhabditis elegans.										
Caenorhabditis elegans.										
Eukaryote; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae										
1 Rhabditidae; Pelodoriinae; Caenorhabditis.										
1 (bases 1 to 500)										
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.										
and Sugeno,S.										
A complementary view of the C.elegans genome										
Unpublished (2002)										
Contact: Tadasi Shin-I										
Center For Genetic Resource Information										
National Institute of Genetics										
1111 Yata, Mishima, Shizuoka 411-8540, Japan										
Tel: 81-559-81-6856										
Fax: 81-559-81-6855										
Email: tshin@genetics.nig.ac.jp.										
Location/Qualifiers										
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subsequent generation of CDNA's by poly(A) priming. The										
CDNA's were cloned into pPC86"										
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156 a										
100 c										
102 g										
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Best Local Similarity										
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Thu Mar 6 08:14:03 2003

us-09-993-420a-1.rst

Page 10

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VERSION        AV190122.1  GI:5572105
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                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
                ; Rhabditidae; Pelodermidae; Caenorhabditis.
REFERENCE      1 (bases 1 to 360)
AUTHORS        Kohara,Y., Shin,I.T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H.,
                Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
                M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
                Nomoto,H.
TITLE          Expressed genes in C.elegans
JOURNAL        Unpublished (1999)
COMMENT        Contact: Yuji Kohara
                Genome Biology Lab.
                National Institute of Genetics
                Yata 1111, Mishima, Shizuoka 411, Japan
                Tel: 81-559-81-6854
                Fax: 81-559-81-6855
                Email: ykohara@lab.nig.ac.jp.
                Location/Qualifiers
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QY 1028 CCAAGATCGCCCAATCGCTCCACATCTACCGTCTACCAAGCCCAATGACCTGGATGC 1087
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QY 1088 TCTCCGATTCCTAATGATCAGCGGTTGTATATGCGCGAACCCTTCTCGTGGAGGAA 1147
DB 163 TCTCCGATTCCTAATGATCAGCGGTTGTATATGCGCGAACCCTTCTCGTGGAGGAA 222
QY 1148 TCGGATTCGCGATTTTCCGCTTGATTCACCGCTTTTGATTCATCCGTAAGCTGGA 1207
DB 223 TCGGATTCGCGATTTTCCGCTTGATTCACCGCTTTTGATTCATCCGTAAGCTGGA 282
QY 1208 ACTTACCATCGCGGTACCGGTGTCTTCAAGTACATCATTTGCTTCCCATATTTCC 1267
DB 283 ACTTACCATCGCGGTACCGGTGTCTTCAAGTACATCATTTGCTTCCCATATTTCC 342
QY 1268 ATACTCTTAACGGAATTC 1285
DB 343 ATACTCTTAACGGAATTC 360
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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 18:37:30 ; Search time 3219.62 Seconds

(without alignments)
11886.551 Million cell updates/sec

Title: US-09-993-420a-2

Perfect score: 1315

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: gb_vl:*
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32: em_hcg_other:*
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41: em_hgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	632.6	48.1	7035	3	CELCYT1A	L26545 Caenorhabditis
2	632.6	48.1	33477	3	CELCYT1A	L26545 Caenorhabditis
3	177.4	13.5	3419	3	CELCBHO	L26545 Caenorhabditis
4	81.8	6.2	7218	6	I66494	Sequence 14
5	55.6	4.2	7218	6	I66494	Sequence 14
6	54.6	4.2	146383	2	AC116367	Sequence 14
7	50.8	3.9	167264	2	AC095776	Sequence 14
8	47.6	3.6	289	6	ARI62089	Sequence 14
9	47.6	3.6	289	6	ARI66614	Sequence 14
10	46.4	3.5	107731	2	AC005476	Sequence 14
11	46.4	3.5	136551	2	AC048354	Sequence 14
12	46.4	3.5	229422	2	AC097544	Sequence 14
13	45.8	3.5	242336	2	AC097416	Sequence 14
14	45.4	3.5	170005	2	AC106291	Sequence 14
15	45.2	3.4	101509	2	AC027353	Sequence 14
16	45	3.4	88827	2	AC103497	Sequence 14
17	44.8	3.4	96102	8	F22D1	Sequence 14
18	44	3.3	151663	2	AC102402	Sequence 14
19	44	3.3	170047	2	AC091947	Sequence 14
20	43.6	3.3	220114	2	AL731767	Sequence 14
21	43.2	3.3	95892	2	AC103202	Sequence 14
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23	42.8	3.3	143301	2	AC095156	Sequence 14
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29	42.4	3.2	180889	2	AC079986	Sequence 14
30	42.4	3.2	193643	9	AC018644	Sequence 14
31	42.2	3.2	63847	2	AC101459	Sequence 14
32	42.2	3.2	125020	9	AF429315	Sequence 14
33	42.2	3.2	142142	2	AC091173	Sequence 14
34	42.2	3.2	186676	9	AC067881	Sequence 14
35	42.2	3.2	215528	2	AC099105	Sequence 14
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37	42	3.2	35409	3	CEC44C10	Sequence 14
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39	42	3.2	166197	2	AC114704	Sequence 14
40	41.8	3.2	224312	2	AL606969	Sequence 14
41	41.6	3.2	2811	8	ATAP72GEN	Sequence 14
42	41.6	3.2	115666	2	AC105744	Sequence 14
43	41.6	3.2	116905	8	AC009322	Sequence 14
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ALIGNMENTS

RESULT 1
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DEFINITION CELCYT1A
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VERSION L26545
KEYWORDS complete cds, and unknown gene.
SOURCE L26545.1 GI:433174
ORGANISM Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 7035)
AUTHORS Hengartner,M.O. and Horvitz,H.R.
TITLE C. elegans cell survival gene ced-9 encodes a functional homolog of

QY 729 AAAAGTGGACCGCGGACAGACAGACGATGATGATGGCGCTGAGTAACAGC 788
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 Db 3930 AAAAGTGGACCGCGGACAGACAGACGATGATGATGGCGCTGAGTAACAGC 3989
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 QY 789 TGGAGCATTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 848
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 QY 909 TTGCTCACTGATTTCTTCATCTTTGAACTGGAAGATGGGAAGCTAGGCCAAT 968
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 Db 4110 TTGCTCACTGATTTCTTCATCTTTGAACTGGAAGATGGGAAGCTAGGCCAAT 4169
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 QY 969 TACGGCTCTCTGTCGATTTACGATTTTACGCAATTTTCCGATTTGCTTTT 1028
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 Db 4170 TACGGCTCTCTGTCGATTTACGATTTTACGCAATTTTCCGATTTGCTTTT 4229
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 QY 1029 GGCACAAACCTTACTCCGCGTATATCACTTTTCCGTTCTGTACATTTGTCANAA 1088
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 Db 4230 GGCACAAACCTTACTCCGCGTATATCACTTTTCCGTTCTGTACATTTGTCANAA 4289
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 QY 1089 CCTCAAAACCTTACTTTTTCGCGGTGCTAGCCTCCGCTCTCTTCCACATTTCCA 1148
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 Db 4290 CCTCAAAACCTTACTTTTTCGCGGTGCTAGCCTCCGCTCTCTTCCACATTTCCA 4349
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 QY 1149 AAGTACCCCTGATTCATTAATTCATTCATTTTCTTCTTCTTCTTCTTCTTCTT 1208
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 Db 4410 TTCCAACTCCCGCCCAATTTCTGTACGCGTATATCACTTTTCTTCTTCTTCTTCTT 4469
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 QY 1269 GTTTCTCTCTAC 1301
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 Db 4470 GTTTCTCTCTAC 4502
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RESULT 2
 CEN07C4 33477 bp DNA linear INV 11-DEC-2001
 LOCUS CEN07C4
 DEFINITION Caenorhabditis elegans cosmid T07C4, complete sequence.
 ACCESSION Z29443
 VERSION Z29443.1 GI:1067051
 KEYWORDS HTG.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
 1 none.
 REFERENCE 1
 AUTHORS Genome sequence of the nematode C. elegans: a platform for
 TITLE investigating biology. The C. elegans Sequencing Consortium
 JOURNAL Science 282 (5396), 2012-2018 (1998)
 MEDLINE 99069613
 PUBMED 9851916
 REMARK The C. elegans Sequencing Consortium.
 REFERENCE 2 (bases 1 to 33477)
 AUTHORS Berts, M.
 TITLE Direct Submission
 JOURNAL Submitted (18-JAN-1994) Nematode Sequencing Project, Sanger
 Institute, Hinxton, Cambridge CB10 1SA, England and Department of
 Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
 jlesanger@ac.uk or trenomacode.wustl.edu
 On Nov 21, 1995 this sequence version replaced gi:443827.
 Coding sequences below are predicted from computer analysis, using
 predictions from GeneFinder (P. Green, U. Washington), and other
 available information.
 COMMENT Current sequence finishing criteria for the C. elegans genome

sequencing consortium are that all bases are either sequenced
 unambiguously on both strands, or on a single strand with both a
 dye primer and dye terminator reaction, from distinct subclones.
 Exceptions are indicated by an explicit note.
 IMPORTANT: This sequence is not the entire insert of clone T07C4.
 It may be shorter because we only sequence overlapping sections
 once, or longer because we arrange for a small overlap between
 neighbouring submissions.
 The true left end of clone T07C4 is at 1 in this sequence. The true
 left end of clone C38H2 is at 33374 in this sequence. The true
 right end of clone T07A5 is at 8844 in this sequence. The start
 of this sequence (1..101) overlaps with the end of sequence 248055.
 The end of this sequence (33374..33477) overlaps with the start of
 sequence 235641.
 For a graphical representation of this sequence and its analysis
 see: [http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?](http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=T07C4)
 name=T07C4
 IMPORTANT: This sequence is NOT necessarily the entire insert of
 the specified clone. It may be shorter because we only sequence
 overlapping sections once, or longer because we arrange for a small
 overlap between neighbouring submissions.
 location/Qualifiers

FEATURES

source

1..33477
 /organism="Caenorhabditis elegans"
 /db_xref="taxon:6239"
 /chromosome="III"
 /clone="T07C4"

gene

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 248055.1:25093..25158,248055.1:25222..25393,
 248055.1:25445..25767,248055.1:25842..25982,
 248055.1:26303..27073,248055.1:27419..28272,102..285,
 385..524,913..1219,1307..1393)
 /gene="T07C4.10a"

CDS

join(248055.1:23123..23168,248055.1:23234..23359,
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 248055.1:25445..25767,248055.1:25842..25982,
 248055.1:26303..27073,248055.1:27419..28272,102..285,
 385..524,913..1219,1307..1393)
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/note="similarity to yeast heat shock protein H104 (Swiss
 port accession number P31359)
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 CDNA EST YK681C11.3 comes from this gene
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 CDNA EST YK681C11.3 comes from this gene
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 CDNA EST YK681C11.5 comes from this gene"

/protein_id="CAA82580.1"
 /db_xref="GI:3979903"
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/translation="MSQKTEPDIDPLADDDPTVITISGCTPRRAOPLPKPEPPDE
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 TSTPRGKSRSMKLENFATFRNDLSTISTGSDTENDSHVLDGVSLAESEKLR
 KDRANSLRDQNSLRGENESLRGENESLRGENESLRGENESLRGENESLRGENESLR
 IDPIVKSSEQIKKELLSFKINDEBRTIMEFAEMMLSDPKPAKVTATATQVNT
 EMDANIOTDKDHNVANANQLEVDLSEIEVYIKKSDLENRLDYETKAAOE
 ODENLRADLEKIKTSQEKLYVYKGIIEELSRNKRKRLKLEVOAENRKLIDKNT
 HDPELRADKVGGEHLEKORKEAMEVBELOLMGLRLBELDRQELKIQLRKMEILR
 KEHEGQMALEKRLKESKEKEALEBQELKQKEMKTVKRENVLSERKQVLLSEDLR
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 RDIDRIGEYIRSEANNELERLKIDAEOKELKLEAMEMARSDLEADLPKRLK
 AREHEFEINARNOFVAVTGMEDIESEYORLLELEPYGPKTIISGFRPSCQTP
 SPATDAMQTDVDEBOLMVSPVSLVSPASLODSRSSHLDKIKRTIKETIELLA
 EHESQESLRDPERFRTAARFKISQLKSLISLGSANSEMERITWTWLTLYKALVEQ
 DEQMKVQKAGMILSQRKESQNEVYTKRSLMEAAEERITVYMDLTKALEVQD
 RIVQDETRREVSSNSTKIEKLEBQEOAHQHELEKRRKREYMKLQKDEYFIMDN
 VKETEENKRLRLKRTEDKERMDPMLIRKAOQKMYLIRKRNQORTSMNNLESVK
 KKIHESRDMNNLQRFEDSIRKYGAELTTEELIEPSSSSSSRTLSNH"

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 5562..5658,6234..6278))

gene

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 248055.1:25445..25767,248055.1:25842..25982,
 248055.1:26303..27073,248055.1:27419..28272,102..285,
 385..524,913..1219,1307..1393)
 /gene="T07C4.10a"

CDS

join(248055.1:23123..23168,248055.1:23234..23359,
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 248055.1:25445..25767,248055.1:25842..25982,
 248055.1:26303..27073,248055.1:27419..28272,102..285,
 385..524,913..1219,1307..1393)
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intron	2132. .2187	/gene="ced-9"	/number=2	2138. .2337	/gene="ced-9"	/number=3
exon	2338. .2550	/gene="ced-9"	/number=3	2551. .2703	/gene="ced-9"	/number=4
intron	2703. .2703	/gene="ced-9"	/number=4			
BASE COUNT	976 a	727 c	668 g	1035 t	13 others	
ORIGIN						
Query Match	13.5%;	Score 177.4;	DB 3;	Length 3419;		
Best Local Similarity	65.1%;	Pred. No. 5.2e-39;				
Matches 308; Conservative	0;	Mismatches 111;	Indels 54;	Gaps 1		
QY 252	ATTGTGTGTCGACTATTTCACGACCGCAATCCGCAAAAGCAATGATGTTGGAGC	311				
DB 1866	ATTTAAGCTTGACTATTTCACATATGCAATGACACAAAATGCTAGATTGTGATGTC	1925				
QY 312	ACCGGATTCGCCGTGTGAGTGCACCCGAGCAGCAAAATGATCGAGTATGSGAAGCAT	371				
DB 1926	GCTTGCAATTACCGGATGAGGTTCAAAAAGCAGTATGATGATCGATCATTTGGSAACGAT	1985				
QY 372	ATTGGAACAACACACCGGAAAATTTTGAGACCTTCTGTGAGCAGCTGCTCGCAGTGCC	431				
DB 1986	TTTTCGAAAAAAGACACATGAGAGTGTTCGAAAACTTCTGTGAAACACTACTTGCAGTTCC	2045				
QY 432	CAGAAATCTCAATTTTCACTGATCAGATGTGGTTCGACGGTTGGAATGCACAGACAGA	491				
DB 2046	AAAAATAGCTTTTTCATTGTACCAAGAAAGTGTGACAGACTGTGSAATTCATCAACAC	2105				
QY 492	TCAATGTCCAATGCTTATGACGTTT	518				
DB 2106	ACGGTGTCAATGCTTATGAGACGTTTGGTAGTTGATCTACAGTGTGATTCATTAAGT	2165				
QY 519	-----GATAGGTCTAATCTCGTTGGCGGTTTCGTAGCTGCAAA	557				
DB 2166	AGTACAGTGTCAATATTTTTCAGATAGGTCTAATTTCCCTTCGAGGAATGGTCTCGCAA	2225				
QY 558	AATGATGGAATCCGTGGAAGTCTCAGAGCAAAAGTGGAAACCTCTTGTTAACACATCGCT	617				
DB 2226	AATGATGGAATCGCTGCTGACTACTCAAAAGGCAAGTGGCAAACTCTTATGTACATATGCT	2285				
QY 618	GTTTCATCAAAACGCGGATCCGCAACACTGGAAGGAAACACATCGAGCTGGG	670				
DB 2286	GTTTCATCAAAACGAGATCCGACAGTCTGTGGAAGAAACACATCGTGTGGG	2338				
RESULT 4						
LOCUS	166494	7218 bp	DNA	linear	PAT 28-DEC-1997	
DEFINITION	Sequence 14 from patent US 5670367.					
ACCESSION	166494					
VERSION	166494.1	GI:2724471				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 7218)					
AUTHORS	Dorner, F., Scheifflinger, F., and Falkner, F. Gunter.					

[illegible]

10

JOURNAL	Direct Submission
TITLE	Unpublished
REFERENCE	2 (bases 1 to 167264)
AUTHORS	Worley,K.C.
JOURNAL	Direct Submission
TITLE	Submitted (17-SEP-2001)
AUTHORS	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (bases 1 to 167264)
AUTHORS	Worley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (11-JUL-2002)
REFERENCE	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	On Jul 10, 2002 this sequence version replaced gi:20975899.

Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homai,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolyet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kurshil,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,M., Loucsged,H.,
Locado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapa,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., McWhiney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabhat,K., Morgan,M., Morris,S.,
Mosier,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nokinewo,S., Oguh,M., Okunnu,G.,
Orgunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickers,R., Primus,E., Pul,L., Quiles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
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Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H.,
Sulton,A., Swatek,A., Tabot,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tamsen,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 167264)
Moriy,K.C.

Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 167264)
Moriy,K.C.

Direct Submission
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:20975899.

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GDHN
Center clone name: CH230-9K20
Sequencing vector: piasmtd;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 99661 bases at least Q40
Consensus quality: 104971 bases at least Q30
Consensus quality: 108925 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_drift_data.html)
NOTE: This is a 'working draft' sequence. It currently
consists of 74 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1
1108: contig of 1108 bp in length
1109
1209: gap of unknown length
1209
2405: contig of 1197 bp in length
2406
2505: gap of unknown length
2506
3645: contig of 1140 bp in length
3646
3745: gap of unknown length
3746
5337: contig of 1592 bp in length


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QY 1006 TTTTCCGATTCCTTTTGGCCAAACCTTCCGCGTAATACACTTTCCG 1065
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Db 287 TTTTCTGTACATTTGTCGCAAAACCTTAACTTTTCTGCGCGCTACCTT 228
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Db 167 YNSYNNYSYNNYSYNNYSYNNYSYNNYSYNNYSYNNYSYNNYSYNN 108
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RESULT 9
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LOCUS Sequence 17 from patent US 6281344.
DEFINITION ARI6614
ACCESSION ARI6614
VERSION ARI6614.1 GI:16242009
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 289)
AUTHORS Sztosik, J.W., Roberts, R.W. and Liu, R.
TITLE Nucleic acid/protein fusion molecules and libraries
JOURNAL Patent: US 6281344-A 17 28-AUG-2001;
FEATURES
source location/Qualifiers
1..289
BASE COUNT 41 a 13 c 9 g 15 t 211 others
ORIGIN
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Query Match 3.6%; Score 47.6; DB 6; Length 289;
Best Local Similarity 11.7%; Pred. No. 0.03;
Matches 32; Conservative 107; Mismatches 135; Indels 0; Gaps 0;

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Db 227 YGCTGTGYSYNNYSYNNYSYNNYSYNNYSYNNYSYNNYSYNNYSYNN 168
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RESULT 10
AC005476 107731 bp DNA linear PRI 09-MAY-2001
LOCUS Homo sapiens PAC clone RPI-261D10 from 14q24.3, complete sequence.
ACCESSION AC005476
VERSION AC005476.4 GI:14010899
KEYWORDS HTG.

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SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 107731)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 107731)
AUTHORS Nelson, D., Kalicki, J. and Miller, R.
TITLE The sequence of Homo sapiens PAC clone RPI-261D10
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 107731)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 107731)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 107731)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (09-MAY-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On May 9, 2001 this sequence version replaced g1:5792183.

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@watson.wustl.edu
----- Summary Statistics -----
Center project name: H_DU0261D10

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
This clone from chromosome 14 was provided by Dr. Pieter de Jong, Roswell Park Cancer Institute, Human Genetics Department, Elm and Carlton Streets, Buffalo NY 14263-0001 USA.

SOURCE INFORMATION:
This clone was derived from human PAC library RPCI-1, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc. (<http://www.genomesystems.com>) or Research Genetics, Inc. (<http://www.resgen.com>); or from Pieter de Jong.

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP6-91H6, 200 bp overlap. Actual clone sequenced to the right is RP6-91H6, 200 bp overlap. Actual start of this clone is at base position 49764 of RP6-116J24; actual

FEATURES	end is at base position 14951 of RP6-91H8.
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	/map="14q24.3"
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	/clone_lib="RC1-1"
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repeat_region	140..430
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repeat_region	1144..1428
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repeat_region	1433..1462
repeat_region	/rpt_family="(CAGA)n"
repeat_region	1514..1570
repeat_region	/rpt_family="MIR"
repeat_region	1610..1786
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repeat_region	2029..2267
repeat_region	/note="match to EST AI940527 (NID:95687508)"
repeat_region	2591..2710
repeat_region	/rpt_family="L2"
repeat_region	3552..3686
repeat_region	/rpt_family="L1"
repeat_region	3687..4002
repeat_region	/rpt_family="Alu"
repeat_region	4003..4499
repeat_region	/rpt_family="L1"
repeat_region	5052..5288
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repeat_region	5469..5586
repeat_region	/rpt_family="MIR"
repeat_region	6139..6227
repeat_region	/rpt_family="MIR"
repeat_region	6343..6652
repeat_region	/rpt_family="Alu"
repeat_region	6967..7278
repeat_region	/rpt_family="Alu"
repeat_region	7360..7460
repeat_region	/rpt_family="MER1_type"
repeat_region	8048..8292
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repeat_region	/rpt_family="MALR"
repeat_region	8657..8720
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repeat_region	9506..9793
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repeat_region	10691..10988
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repeat_region	14137..14165
repeat_region	/rpt_family="(TTTTTG)n"
repeat_region	14683..15198
repeat_region	/rpt_family="L1"
repeat_region	14969..14971
repeat_region	/note="similar to EST AA146730 (NID:91719241) z144a10.s1

Query Match	3.5%	Score 46.6;	DB 9;	Length 107731;
Best Local Similarity	52.4%	Pred. No. 0.15;		
Matches 100;	Conservative	1;	Mismatches 90;	Indels 0;
Gaps	0;			
QY 832 ATGTTGAGCTTGAAGTAACGATATTCATTTTGTGTAATAATTAATTAATGATACACACCTG 891				
Db 3335 AAGTTGAGTATTAATAAAGTACTCTCTTCCATCATATATGATTAAGTTAACTACACAGACT 3394				
QY 892 TACATTTGATATTCATTTTGGTCGCACTGATCTCTCATCTCTTAACTGAGAGAAGTGG 951				
Db 3395 TTACACGACATTTTCTTCTGCTGATCAACGACACATGCTTCCAGATGAAATCTTGA 3454				
QY 952 AAAGCTAGGCGACAAATTAACGGCTCTCTGTGCGATTTTACGATTTTACTGCAATTTTTC 1011				
Db 3455 AAAGCCAAAGACTGACATTAACCTTGATTTTGGATTTTCAATTAACCTTCACTTCATC 3514				
QY 1012 CGATTTGCCCTTT 1022				
Db 3515 AACATCTCTTT 3525				

NOTE: This record contains 92 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allow overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

1	1019:	contig of 1019 bp in length
*		gap of unknown length
*	1020	1802: contig of 783 bp in length
*		gap of unknown length
*	1803	2807: contig of 1005 bp in length
*		gap of unknown length
*	2808	3822: contig of 1015 bp in length
*		gap of unknown length
*	3823	5250: contig of 1428 bp in length
*		gap of unknown length
*	5251	6271: contig of 1021 bp in length
*		gap of unknown length
*	6272	7554: contig of 1283 bp in length
*		gap of unknown length
*	7555	8338: contig of 784 bp in length
*		gap of unknown length
*	8339	9477: contig of 1139 bp in length
*		gap of unknown length
*	9478	10267: contig of 790 bp in length
*		gap of unknown length
*	10268	11090: contig of 823 bp in length
*		gap of unknown length
*	11091	12157: contig of 1067 bp in length
*		gap of unknown length
*	12158	12867: contig of 810 bp in length
*		gap of unknown length
*	12968	13772: contig of 805 bp in length
*		gap of unknown length
*	13773	14990: contig of 1218 bp in length
*		gap of unknown length
*	14991	15111: contig of 121 bp in length
*		gap of unknown length
*	15112	16080: contig of 969 bp in length
*		gap of unknown length
*	16081	16892: contig of 812 bp in length
*		gap of unknown length
*	16893	17821: contig of 929 bp in length
*		gap of unknown length

*	17822	18526:	contig of 705 bp in length
*		gap of unknown length	
*	18527	19587:	contig of 1061 bp in length
*		gap of unknown length	
*	19588	20684:	contig of 1097 bp in length
*		gap of unknown length	
*	20685	21449:	contig of 765 bp in length
*		gap of unknown length	
*	21450	22430:	contig of 961 bp in length
*		gap of unknown length	
*	22431	23323:	contig of 893 bp in length
*		gap of unknown length	
*	23324	24068:	contig of 745 bp in length
*		gap of unknown length	
*	24069	24828:	contig of 760 bp in length
*		gap of unknown length	
*	24829	25757:	contig of 929 bp in length
*		gap of unknown length	
*	25758	26813:	contig of 1056 bp in length
*		gap of unknown length	
*	26814	27836:	contig of 1023 bp in length
*		gap of unknown length	
*	27837	28912:	contig of 1076 bp in length
*		gap of unknown length	
*	28913	29839:	contig of 927 bp in length
*		gap of unknown length	
*	29840	30811:	contig of 972 bp in length
*		gap of unknown length	
*	30812	31909:	contig of 1098 bp in length
*		gap of unknown length	
*	31910	33295:	contig of 1386 bp in length
*		gap of unknown length	
*	33296	34683:	contig of 1388 bp in length
*		gap of unknown length	
*	34684	36215:	contig of 1532 bp in length
*		gap of unknown length	
*	36216	37454:	contig of 1239 bp in length
*		gap of unknown length	
*	37455	39106:	contig of 1652 bp in length
*		gap of unknown length	
*	39107	40369:	contig of 1263 bp in length
*		gap of unknown length	
*	40370	41799:	contig of 1430 bp in length
*		gap of unknown length	
*	41800	43877:	contig of 2078 bp in length
*		gap of unknown length	
*	43878	45004:	contig of 1127 bp in length
*		gap of unknown length	
*	45005	46454:	contig of 1450 bp in length
*		gap of unknown length	
*	46455	47458:	contig of 1004 bp in length
*		gap of unknown length	
*	47459	48594:	contig of 1136 bp in length
*		gap of unknown length	
*	48595	49351:	contig of 757 bp in length
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*	49352	50486:	contig of 1135 bp in length
*		gap of unknown length	
*	50487	51205:	contig of 719 bp in length
*		gap of unknown length	
*	51206	52428:	contig of 1223 bp in length
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*	52429	53679:	contig of 1251 bp in length
*		gap of unknown length	
*	53680	54609:	contig of 930 bp in length
*		gap of unknown length	
*	54610	55895:	contig of 1286 bp in length
*		gap of unknown length	
*	55896	57444:	contig of 1549 bp in length
*		gap of unknown length	
*	57445	58912:	contig of 1468 bp in length
*		gap of unknown length	
*	58913	60270:	contig of 1358 bp in length

COMMENT

of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:17973416.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project name: GHMB

Center clone name: CH230-10207

Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 158574 bases at least Q40

Consensus quality: 164750 bases at least Q30

Consensus quality: 169543 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 74 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

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1 1077: contig of 1077 bp in length
* 1078 1177: gap of unknown length
* 1178 2279: contig of 1102 bp in length
* 2280 2379: gap of unknown length
* 2380 3440: contig of 1061 bp in length
* 3441 4654: gap of unknown length
* 4655 4755: gap of unknown length
* 4755 5839: contig of 1085 bp in length
* 5840 5939: gap of unknown length
* 5940 7595: contig of 1656 bp in length
* 7596 7696: gap of unknown length
* 7696 8853: contig of 1158 bp in length
* 8854 8954: gap of unknown length
* 8954 10166: contig of 1212 bp in length
* 10166 10265: gap of unknown length
* 10265 11745: contig of 1480 bp in length
* 11746 11845: gap of unknown length
* 11846 12848: contig of 1003 bp in length
* 12849 12948: gap of unknown length
* 12949 14505: contig of 1557 bp in length
* 14506 14605: gap of unknown length
* 14606 15923: contig of 1318 bp in length
* 15924 16023: gap of unknown length
* 16024 17271: contig of 1248 bp in length
* 17272 17371: gap of unknown length
* 17372 18474: contig of 1103 bp in length
* 18475 18574: gap of unknown length
* 18575 19720: contig of 1146 bp in length
* 19721 19820: gap of unknown length
* 19821 21097: contig of 1277 bp in length
* 21098 21197: gap of unknown length
* 21198 22523: contig of 1326 bp in length
* 22524 22623: gap of unknown length
* 22624 23810: contig of 1187 bp in length
* 23811 23910: gap of unknown length
* 23911 24943: contig of 1032 bp in length
* 24943 25043: gap of unknown length
* 25043 26557: contig of 1614 bp in length
* 26557 26757: gap of unknown length
* 26757 27846: contig of 1090 bp in length
* 27846 27947: gap of unknown length
* 27947 29722: contig of 1776 bp in length
* 29723 29822: gap of unknown length
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29823 31366: contig of 1544 bp in length
* 31367 31466: gap of unknown length
* 31467 33202: contig of 1736 bp in length
* 33203 33302: gap of unknown length
* 33303 34984: contig of 1692 bp in length
* 34985 35094: gap of unknown length
* 35095 36771: contig of 1677 bp in length
* 36772 38806: contig of 1935 bp in length
* 38807 38907: gap of unknown length
* 38907 40645: contig of 1739 bp in length
* 40646 40745: gap of unknown length
* 40746 42406: contig of 1721 bp in length
* 42407 42566: gap of unknown length
* 42567 44744: contig of 2178 bp in length
* 44745 44844: gap of unknown length
* 44845 46935: contig of 2091 bp in length
* 46936 47035: gap of unknown length
* 47036 49255: contig of 2220 bp in length
* 49256 49355: gap of unknown length
* 49356 50767: contig of 1412 bp in length
* 50768 50867: gap of unknown length
* 50868 52218: contig of 1351 bp in length
* 52219 52319: gap of unknown length
* 52319 53853: contig of 1535 bp in length
* 53854 53954: gap of unknown length
* 53954 56201: contig of 2248 bp in length
* 56202 56301: gap of unknown length
* 56301 58728: contig of 2427 bp in length
* 58729 58828: gap of unknown length
* 58829 60272: contig of 1443 bp in length
* 60272 60372: gap of unknown length
* 60372 62519: contig of 2147 bp in length
* 62519 62619: gap of unknown length
* 62619 66044: contig of 3425 bp in length
* 66044 66144: gap of unknown length
* 66144 68947: contig of 2804 bp in length
* 68947 69047: gap of unknown length
* 69048 71619: contig of 2571 bp in length
* 71619 71719: gap of unknown length
* 71719 74043: contig of 2325 bp in length
* 74044 74143: gap of unknown length
* 74144 76423: contig of 2180 bp in length
* 76423 76424: gap of unknown length
* 76424 78434: contig of 2010 bp in length
* 78434 78534: gap of unknown length
* 78534 80018: contig of 1484 bp in length
* 80018 80117: gap of unknown length
* 80117 82845: contig of 2728 bp in length
* 82845 82945: gap of unknown length
* 82946 86645: contig of 3700 bp in length
* 86646 86745: gap of unknown length
* 86746 89688: contig of 2923 bp in length
* 89689 89768: gap of unknown length
* 89769 92784: contig of 3016 bp in length
* 92785 92884: gap of unknown length
* 92885 96529: contig of 3645 bp in length
* 96530 96630: gap of unknown length
* 96630 99446: contig of 2817 bp in length
* 99447 99547: gap of unknown length
* 99547 103361: contig of 3815 bp in length
* 103362 103362: gap of unknown length
* 103362 108371: contig of 4910 bp in length
```

Query Match

Best Local Similarity 43.18; Score 46; DB 2; Length 229422;
Matches 88; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

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OY 1110 CGCGGTGGCCCTACCTCCGCTTCTTCCACATTTCCAAAGTACCGCTGATCTCATA 1169
Db 1978 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
OY 1170 ATTCACTTCACTTAACTGCTCTTTTGTGTGCGCTTTCACACTCCGCCCAATTC 1229
```

[illegible]

REFERENCE	Baylor Plaza, Houston, TX 77030, USA
AUTHORS	3 (bases 1 to 242336)
TITLE	Worley, K.C.
JOURNAL	Direct Submission Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2002 this sequence version replaced gi:17973592.
COMMENT	----- Genome Center Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ----- Project Information Center project name: GICX Center clone name: CH230-192C3 ----- Summary Statistics Sequencing vector: plasmid: Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 73499 bases at least Q40 Consensus quality: 78275 bases at least Q30 Consensus quality: 83602 bases at least Q20 ----- * NOTE: Estimated insert size may differ from sequence length * (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html) * NOTE: This is a 'working draft' sequence. It currently * consists of 140 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. 1 1009: contig of 1009 bp in length 1010 1109: gap of unknown length 1110 2236: contig of 1127 bp in length 2237 2336: gap of unknown length 2337 3388: contig of 1052 bp in length 3389 3488: gap of unknown length 3489 4660: contig of 1172 bp in length 4661 4760: gap of unknown length 4761 5777: contig of 1017 bp in length 5778 5877: gap of unknown length 5879 7036: contig of 1159 bp in length 7037 7136: gap of unknown length 7137 8162: contig of 1026 bp in length 8163 8262: gap of unknown length 8263 9364: contig of 1102 bp in length 9365 9464: gap of unknown length 9465 11357: contig of 1893 bp in length 11358 11457: gap of unknown length 11458 12535: contig of 1078 bp in length 12536 12635: gap of unknown length 12636 14100: contig of 1465 bp in length 14101 14200: gap of unknown length 14201 15554: contig of 1354 bp in length 15555 15654: gap of unknown length 15655 17062: contig of 1408 bp in length 17063 17162: gap of unknown length 17163 18321: contig of 1159 bp in length 18321 18421: gap of unknown length 18422 19649: contig of 1228 bp in length 19650 19749: gap of unknown length 19750 20936: contig of 1187 bp in length 20937 21036: gap of unknown length 21037 22163: contig of 1127 bp in length 22164 22663: gap of unknown length 22664 23397: contig of 1134 bp in length 23397 23497: gap of unknown length 23498 24532: contig of 1035 bp in length 24533 24632: gap of unknown length 24633 25783: contig of 1151 bp in length

OY	1167	AATATTACTCTACGTTTAACTGTCTCTTTTGCGTGGCCCTTCACAATCCCCCAAT	1226
Db	98441	ATAATTATTTTTTTTTTTTTTTTGTGTTTTTTTTTTTTNNNCCCNNCCCCCCCCC	98382
OY	1227	TCTGTAGCGCATCGGCATCTGTGAATTAATTTTTTTCAAATGTGTTCTCTACACAA	1286
Db	98381	CCNCGCCNNNGNGTGNTGGTGTTTTTTTTTTTTTTTTTTAATCTCCANAAAA	98322
OY	1287	CAAAAAAAAAAGGTCCAIAAAAAAAAAAAAA	1315
Db	98321	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	98293

RESULT 14					
AC106291	AC106291	170005 bp	DNA	linear	HTG 13-JUL-2007
LOCUS	Rattus norvegicus clone CH230-72c9,	***	SEQUENCING IN PROGRESS	***,	
DEFINITION	71 unordered pieces.				
ACCESSION	AC106291				
VERSION	AC106291.2	GI:21731640			
KEYWORDS	HTG; HTGS_PHASE1.				
SOURCE	Norway rat.				
ORGANISM	Rattus norvegicus				

REFERENCE
AUTHORS

REFERENCE	1 (bases 1 to 170005)
Altshuler	13

ΣΥΝΟΠΤΟΥ

REFERENCE

AUTHORS

1 (bases 1 to 170005)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

Muzny,D.M., Adams,C., Adio-Obuola,B., All-oman,F.R., Allen,C.,
Alsbrooks,S.L., Amaral-Jung,H.C., Are,J.R., Ayele,K., Banks,T.,
Barbataki,J., Benton,J., Bimberg,K., Blankenburg,K., Bonani,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Butah,C., Burch,P., Burkett,C., Burrell,K.L., Byrd N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Devila,M.L., Davis,G., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,M., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Hawlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognues,M., Holloway,C., Hollins,B.,
Homsli,F., Howard,S., Huber,J., Hultky,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jollyvet,S., Joudah,S.,
Kallsson,E., Kelly,S., Khan,U., King,L., Korvay,J., Kovar,C.,
Kratovic,J., Kreshl,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,M., Louisgead,H.,
Lozando,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawlinney,E., Mcleod,M.P., Meador,M., Mel,G., Metzger,S.,
Miner,G., Miner,Z., Mitchell,T., Mohabhat,K., Morgan,M., Morris,S.,
Mosser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokwanko,S., Oguh,M., Okunmoy,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pul,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojudo-Kan,I., Rolfe,M., Ruiz,S., Savery,G.,
Schwartz,S., Scott,K., Shen,H., Shooshitari,N., Sisson,I.,
Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Umanal,K., Vasquez,L., Vera,Y., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S.,
Williams,G., Williams,A., Wleciyzk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.P., Zhou,X., Zorrilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.

Query Match	3.5%;	Score 45.8;	DB 2;	Length 242336;
Best Local Similarity	53.7%;	Pred. NO. 0.29;		
Matches	80;	Conservative	0;	Mismatches 69;
			Indels	0;
			Gaps	0;

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 170005)
AUTHORS Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2002) Human Genome Sequencing Center, Department

REFERENCE
AUTHORS
TITLE
JOURNAL

of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 170005)

COMMENT

Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced g1:18139812.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GK01
Center clone name: CH230-72C9

----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye: 1008 of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 113946 bases at least Q40
Consensus quality: 121487 bases at least Q30
Consensus quality: 128156 bases at least Q20

----- NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 71 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of 'N', but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

```

1      1153: contig of 1153 bp in length
*      1154      1253: gap of unknown length
*      1254      2285: contig of 1032 bp in length
*      2286      2385: gap of unknown length
*      2386      3502: contig of 1117 bp in length
*      3503      3602: gap of unknown length
*      3603      5325: contig of 1723 bp in length
*      5326      5425: gap of unknown length
*      5426      6764: contig of 1339 bp in length
*      6765      6864: gap of unknown length
*      6865      7991: contig of 1127 bp in length
*      7992      8091: gap of unknown length
*      8092      9272: contig of 1181 bp in length
*      9273      9373      10833: contig of 1461 bp in length
*      9373      10933: gap of unknown length
*      10834      12391: contig of 1458 bp in length
*      10934      12491: gap of unknown length
*      12392      13515: contig of 1024 bp in length
*      12492      13615: gap of unknown length
*      13516      15639: contig of 2024 bp in length
*      13616      15739: gap of unknown length
*      15640      16903: contig of 1164 bp in length
*      15740      17003: gap of unknown length
*      16904      18570: contig of 1567 bp in length
*      17004      18670: gap of unknown length
*      18571      19958: contig of 1288 bp in length
*      18671      20058: gap of unknown length
*      19959      21386: contig of 1328 bp in length
*      20059      21486: gap of unknown length
*      21387      22588: contig of 1102 bp in length
*      21487      22689: gap of unknown length
*      22689      23779: contig of 1091 bp in length
*      23780      23879: gap of unknown length
*      23880      25557: contig of 1678 bp in length
*      25558      25657: gap of unknown length
*      25658      27550: contig of 1893 bp in length
*      27550      27551: gap of unknown length

```

```

*      27551      29682: contig of 2032 bp in length
*      29683      29782: gap of unknown length
*      29783      31436: contig of 1654 bp in length
*      31437      31536: gap of unknown length
*      31537      32749: contig of 1213 bp in length
*      32750      32849: gap of unknown length
*      32850      34367: contig of 1518 bp in length
*      34368      34467: gap of unknown length
*      34468      35540: contig of 1073 bp in length
*      35541      35640: gap of unknown length
*      35641      37378: contig of 1738 bp in length
*      37379      37478: gap of unknown length
*      37479      40174: contig of 2696 bp in length
*      40175      40275: gap of unknown length
*      40276      42051: contig of 1776 bp in length
*      42052      42151: gap of unknown length
*      42152      43567: contig of 1417 bp in length
*      43568      43667: gap of unknown length
*      43668      44712: contig of 1045 bp in length
*      44713      44812: gap of unknown length
*      44813      45993: contig of 1181 bp in length
*      45994      46094: gap of unknown length
*      46095      47679: contig of 1586 bp in length
*      47680      47779: gap of unknown length
*      47780      49052: contig of 1273 bp in length
*      49053      49152: gap of unknown length
*      49153      50987: contig of 1835 bp in length
*      50988      51087: gap of unknown length
*      51089      53149: contig of 2062 bp in length
*      53150      53249: gap of unknown length
*      53250      54528: contig of 1279 bp in length
*      54529      54628: gap of unknown length
*      54629      56210: contig of 1582 bp in length
*      56211      56310: gap of unknown length
*      56311      58009: contig of 1699 bp in length
*      58010      58109: gap of unknown length
*      58110      60268: contig of 2159 bp in length
*      60269      60368: gap of unknown length
*      60369      62307: contig of 1939 bp in length
*      62308      62407: gap of unknown length
*      62408      63892: contig of 1485 bp in length
*      63893      63992: gap of unknown length
*      63993      66676: contig of 2684 bp in length
*      66677      66776: gap of unknown length
*      66777      68795: contig of 2019 bp in length
*      68796      68895: gap of unknown length
*      68896      71185: contig of 2290 bp in length
*      71186      71285: gap of unknown length
*      71286      73230: contig of 1945 bp in length
*      73231      73330: gap of unknown length
*      73331      76851: contig of 3521 bp in length
*      76852      76951: gap of unknown length
*      76952      79277: contig of 2326 bp in length
*      79278      79377: gap of unknown length
*      79379      82280: contig of 2903 bp in length
*      82281      82380: gap of unknown length
*      82381      85008: contig of 2628 bp in length
*      85009      85108: gap of unknown length
*      85109      87508: contig of 2400 bp in length
*      87509      87608: gap of unknown length
*      87609      91272: contig of 3664 bp in length
*      91273      91372: gap of unknown length
*      91373      93438: contig of 2066 bp in length
*      93439      93538: gap of unknown length
*      93539      96282: contig of 2744 bp in length
*      96283      96382: gap of unknown length
*      96383      99441: contig of 3059 bp in length
*      99442      99542: gap of unknown length
*      99543      102218: contig of 2677 bp in length

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Query Match 3.58; Score 45.4; DB 2; Length 170005;
Best Local Similarity 48.6%; Pred. No. 0.36; Mismatches 125; Indels 0; Gaps 0;
Matches 118; Conservative 0;

[illegible]

*	4872	48871: gap of unknown length
*	48872	50000: contig of 1129 bp in length
*	50001	50100: gap of unknown length
*	50101	51241: contig of 1141 bp in length
*	51242	51341: gap of unknown length
*	51342	52439: contig of 1098 bp in length
*	52440	52539: gap of unknown length
*	52540	53719: contig of 1180 bp in length
*	53720	53819: gap of unknown length
*	53820	54972: contig of 1153 bp in length
*	54973	55072: gap of unknown length
*	55073	56236: contig of 1184 bp in length
*	56237	56356: gap of unknown length
*	56357	57447: contig of 1091 bp in length
*	57448	57547: gap of unknown length
*	57548	58710: contig of 1163 bp in length
*	58711	58810: gap of unknown length
*	58811	59999: contig of 1189 bp in length
*	60000	60099: gap of unknown length
*	60100	61343: contig of 1244 bp in length
*	61344	61443: gap of unknown length
*	61444	62568: contig of 1125 bp in length
*	62568	62668: gap of unknown length
*	62669	63904: contig of 1236 bp in length
*	63905	64004: gap of unknown length
*	64005	65045: contig of 1041 bp in length
*	65046	65145: gap of unknown length
*	65146	66360: contig of 1215 bp in length
*	66361	66460: gap of unknown length
*	66461	67705: contig of 1245 bp in length
*	67706	67805: gap of unknown length
*	67806	68914: contig of 1109 bp in length
*	68915	69014: gap of unknown length
*	69015	70199: contig of 1185 bp in length
*	70200	70299: gap of unknown length
*	70300	71355: contig of 1056 bp in length
*	71356	71455: gap of unknown length
*	71456	73215: contig of 1760 bp in length
*	73216	73315: gap of unknown length
*	73316	74556: contig of 1141 bp in length
*	74557	74656: gap of unknown length
*	74657	76312: contig of 1756 bp in length
*	76313	76412: gap of unknown length
*	76413	77584: contig of 1072 bp in length
*	77585	77584: gap of unknown length
*	77585	78683: contig of 1099 bp in length
*	78684	78783: gap of unknown length
*	78784	79858: contig of 1075 bp in length
*	79859	79958: gap of unknown length
*	79959	80987: contig of 1029 bp in length
*	80988	81087: gap of unknown length
*	81088	82188: contig of 1101 bp in length
*	82189	82288: gap of unknown length
*	82289	83320: contig of 1032 bp in length
*	83321	83420: gap of unknown length
*	83421	84521: contig of 1101 bp in length
*	84522	84622: gap of unknown length
*	84622	101509: contig of 16888 bp in length

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using SW model

Run on: February 27, 2003, 18:35:25 ; Search time 237.618 Seconds
(without alignments)
12462.745 Million cell updates/sec

Title: US-09-993-420a-2

Perfect score: 1315

Sequence: 1 tttagatgacacgtcgtcac.....cgttcaaaaaaaaaaaaaa 1315

Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

1: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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21: /SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1311.4	99.7	1315	AA054630	ced-9 coding seque
2	632.6	48.1	6560	AA054629	Genomic region con
3	44.2	3.4	626	ABV60941	Human prostate exp
4	44.2	3.2	3160	AA158066	Human polynucleoti
5	41.4	3.1	545	AB052458	Oligonucleotide fo
6	41.4	3.1	545	AB052459	Oligonucleotide fo
7	40.2	3.0	411	AA188595	Human polynucleoti
8	39.8	3.0	397	AA182664	Human polynucleoti
9	39.8	3.0	425	AA560450	Human cancer agent

C 10	39.8	3.0	425	22	AA560450	Human cancer agent
C 11	39.6	3.0	458	24	AB193709	Arabidopsis thalia
C 12	39.6	3.0	556	23	ABV40063	Human prostate exp
C 13	39.6	3.0	556	23	ABV40163	Human prostate exp
C 14	39.6	3.0	556	23	ABV42105	Human prostate exp
C 15	39.6	3.0	556	23	ABV43601	Human prostate exp
C 16	39.6	3.0	612	22	AAH71471	Human cervical can
C 17	39.6	3.0	2970	20	AAV20290	Borrelia burgdorfe
C 18	39.4	3.0	426	23	ABV60871	Human prostate exp
C 19	39.4	3.0	1315	21	AA05464	Human secreted pro
C 20	39.4	3.0	1680	21	AA09827	Human secreted pro
C 21	39.4	3.0	8789	23	AB103040	Drosophila melanog
C 22	38.8	2.9	9507	24	ABV61374	Human chemically m
C 23	38.6	2.9	299	23	AA193518	Human prostate exp
C 24	38.6	2.9	408	22	AA193518	Human prostate exp
C 25	38.4	2.9	405	22	AA193518	Human polynucleoti
C 26	38.4	2.9	8323	24	AB132058	Novel human polyn
C 27	38.2	2.9	6222	24	AB132692	Human immune syste
C 28	38	2.9	556	23	ABV40063	Human immune syste
C 29	38	2.9	556	23	ABV40163	Human prostate exp
C 30	38	2.9	556	23	ABV42105	Human prostate exp
C 31	38	2.9	556	23	ABV43601	Human prostate exp
C 32	38	2.9	608	24	AB066317	Human prostate exp
C 33	38	2.9	1542	21	AAA10594	Arabidopsis thalia
C 34	38	2.9	10732	21	AAA10594	DNA encoding a hum
C 35	38	2.9	17848	22	AA545322	Chemically pretrea
C 36	38	2.9	17848	22	ABK39875	Human chemically p
C 37	38	2.9	17848	24	ABK28163	Human transcription
C 38	37.8	2.9	417	21	AA024643	Human secreted pro
C 39	37.8	2.9	3492	23	AB117180	Drosophila melanog
C 40	37.8	2.9	7261	22	AA546669	Tumour suppressor
C 41	37.6	2.9	5432	24	ABN80000	Human chemically m
C 42	37.6	2.9	6031	22	AA546621	Tumour suppressor
C 43	37.4	2.8	278	22	AAH69999	Human cervical can
C 44	37.4	2.8	4590	22	AAH24065	Yeast AOD9604-asso
C 45	37.4	2.8	6229	24	AB132264	Human immune syste

ALIGNMENTS

RESULT 1
AA054630
ID AA054630 standard; cDNA to mRNA: 1315 BP.

XX AA054630;

XX 23-JUN-1994 (first entry)

XX ced-9 coding sequence.

XX Cell death; senescence; programmed cell death; ced-9; myocardial

XX Infarction; stroke; brain injury; neurodegenerative disease;

XX muscular degenerative disease; ageing; hypoxia; ischaemia; toxemia;

XX infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;

XX oncogene; ss.

XX Caenorhabditis elegans.

XX Key

XX CDS

XX 23-DEC-1993.

XX 14-JUN-1993; 93MO-US05651.

XX 12-JUN-1992; 92US-0898933.

XX 10-AUG-1992; 92US-0927681.

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX Hengartner M, Horvitz HR;
 PI WPI: 1994-007540/01.
 DR P-PSDB: AAR47343.
 XX Caenorhabditis elegans cell death-protective gene - used to
 PT develop agents for preventing cell death or for reducing
 PT population of cells
 PS Claim 3: Page 58-59; 112pp: English.
 XX ced-9 is essential for C. elegans development and apparently
 CC functions by protecting cells during development from programmed
 CC cell death. ced-9 was shown to function by antagonising the
 CC activities of cell death genes ced-3 and ced-4. The protein product
 CC of the human oncogene bcl-2 was found to have a similar sequence
 CC to the ced-9 protein. The ced-9 gene can be used for developing
 CC agents for treating a condition characterised by increased cell death
 CC such as myocardial infarction, stroke, traumatic brain injury,
 CC neurodegenerative disease, muscular degenerative disease, ageing,
 CC hypoxia, ischaemia, toxemia, infection or hair loss. It can also
 CC be used for reducing a population of cells in the treatment of
 CC neoplastic growth cancerous tissue, infected cells or autoreactive
 CC immune cells.
 XX SQ Sequence 1315 BP; 362 A; 290 C; 315 G; 347 T; 1 other:
 Query Match 99.7%; Score 1311.4; DB 15; Length 1315;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1313; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 601 TTGCTTACACATCGCTGTTTCATCAAAAACGGGATCCGCAACACTGAGAGACACAT 660
 DB 601 TTGCTTACACATCGCTGTTTCATCAAAAACGGGATCCGCAACACTGAGAGACACAT 660
 QY 661 CGAGCTGGAGACACTTTCATGACACTCGGAAAAAACAATGAAAGAGACTACGACGACA 720
 DB 661 CGAGCTGGAGACACTTTCATGACACTCGGAAAAAACAATGAAAGAGACTACGACGACA 720
 QY 721 GAGCTGAAAAAGTGGGAGCGCGGAAAGCAAGACAGCGGTGTCGATTTGGGCTGGA 780
 DB 721 GAGCTGAAAAAGTGGGAGCGCGGAAAGCAAGACAGCGGTGTCGATTTGGGCTGGA 780
 QY 781 GTAACAGCTGAGACATTTGGAATCGTTGAGAGTCGTCGTGTGGGCGGATGATTTGACG 840
 DB 781 GTAACAGCTGAGACATTTGGAATCGTTGAGAGTCGTCGTGTGGGCGGATGATTTGACG 840
 QY 841 TTGACGTAACGTAATTTGATTTGTTGTAATTAATTTATGTCACACTCTTACATTTGA 900
 DB 841 TTGACGTAACGTAATTTGATTTGTTGTAATTAATTTATGTCACACTCTTACATTTGA 900
 QY 901 ATCTCAATTTTGGCTCACTGATTTCTCATCTTTGAACTGGAAGAAGTGGAAAGCTAGG 960
 DB 901 ATCTCAATTTTGGCTCACTGATTTCTCATCTTTGAACTGGAAGAAGTGGAAAGCTAGG 960
 QY 961 CCACAAATTAACGGCTCTCTGTGTGATTAAGATTTTACGCAATTTTTCGATTTGCT 1020
 DB 961 CCACAAATTAACGGCTCTCTGTGTGATTAAGATTTTACGCAATTTTTCGATTTGCT 1020
 QY 1021 TTTTGTGTCGCAAAACCTTACTTCCGCGTATATCACTTTCCGTTCTGTACATTTTC 1080
 DB 1021 TTTTGTGTCGCAAAACCTTACTTCCGCGTATATCACTTTCCGTTCTGTACATTTTC 1080
 QY 1081 GTCAAAAACCTTAAACCTTAACTTTTCGCGGTGAGTTCGATTTTCGATTTTC 1140
 DB 1081 GTCAAAAACCTTAAACCTTAACTTTTCGCGGTGAGTTCGATTTTCGATTTTC 1140
 QY 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTA 1200
 DB 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTA 1200
 QY 1201 GTGGCCCTTCCAAACCTTCCGCGGTGAGTTCGATTTTCGATTTTC 1260
 DB 1201 GTGGCCCTTCCAAACCTTCCGCGGTGAGTTCGATTTTCGATTTTC 1260
 QY 1261 TTCAAAATTTGTTTCTCTCTCAACAACAAAAAAGGTTTCAAAAAA 1315
 DB 1261 TTCAAAATTTGTTTCTCTCTCAACAACAAAAAAGGTTTCAAAAAA 1315

RESULT 2
 AA054629
 ID AA054629 standard; DNA: 6560 BP.
 XX
 AC AA054629;
 DT 23-JUN-1994 (first entry)
 XX
 DE Genomic region containing ced-9 gene.
 XX
 KW Cell death; senescence; programmed cell death; ced-9; myocardial
 KW infarction; stroke; brain injury; neurodegenerative disease;
 KW muscular degenerative disease; ageing; hypoxia; ischaemia; toxemia;
 KW infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;
 KW oncogene; ss.
 XX
 OS Caenorhabditis elegans.
 XX
 PN WO9325683-A.
 XX
 PD 23-DEC-1993.
 XX
 FE 14-JUN-1993; 93WO-US05651.
 XX

PR 12-JUN-1992; 92US-0898933.
 PR 10-AUG-1992; 92US-0927681.
 XX
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Hengartner M, Horvitz HR;
 DR WPI; 1994-007540/01.
 XX
 PT Caenorhabditis elegans cell death-protective gene - used to
 PT develop agents for preventing cell death or for reducing
 PT population of cells
 XX
 PS Claim 3; Page 54-58; 112pp; English.
 XX
 CC ced-9 is essential for C. elegans development and apparently
 CC functions by protecting cells during development from programmed
 CC cell death. ced-9 was shown to function by antagonising the
 CC activities of cell death genes ced-3 and ced-4. The protein product
 CC of the human oncogene bcl-2 was found to have a similar sequence
 CC to the ced-9 protein. The ced-9 gene can be used for developing
 CC agents for treating a condition characterised by increased cell death
 CC such as myocardial infarction, stroke, traumatic brain injury,
 CC neurodegenerative disease, muscular degenerative disease, aging,
 CC hypoxia, ischaemia, toxemia, infection or hair loss. It can also
 CC be used for reducing a population of cells in the treatment of
 CC neoplastic growth cancerous tissue, infected cells or autoreactive
 CC immune cells.
 XX
 XX Sequence 6560 BP; 2040 A; 1274 C; 1203 G; 2023 T; 20 other;
 SQ
 Query Match 48.1%; Score 632.6; DB 15; Length 6560;
 Best Local Similarity 99.8%; Pred. No. 4.8e-172;
 Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 669 GGACGACTTCATGACACTCGAAGAAACAATGAAAGAGACTACGACAGAGAGAGCTGA 728
 DB 3393 GGACGACTTCATGACACTCGAAGAAACAATGAAAGAGACTACGACAGAGAGCTGA 3452
 QY 729 AAAAGTGGAGCGCGGAGACACAGACAGCGTGCATGATTGGCGCTGGAGTAACAGC 788
 DB 3453 AAAAGTGGAGCGCGGAGACACAGACAGCGTGCATGATTGGCGCTGGAGTAACAGC 3512
 QY 789 TGGAGCATTTGGAGATCGTGGAGTGTGCTGTGGCGGATGATGTTCAAGTTAAAGTA 848
 DB 3513 TGGAGCATTTGGAGATCGTGGAGTGTGCTGTGGCGGATGATGTTCAAGTTAAAGTA 3572
 QY 849 ACGTATTCATTTTGTAAATAATTAAATTATGTAACAACCTCTTACATTTGAATCTCAT 908
 DB 3573 ACGTATTCATTTTGTAAATAATTAAATTATGTAACAACCTCTTACATTTGAATCTCAT 3632
 QY 909 TTGTCGACTGATTCCTCATCCTTTGAAGTGAAGAGTGGGAAGCTAGGCCCAAT 968
 DB 3633 TTGTCGACTGATTCCTCATCCTTTGAAGTGAAGAGTGGGAAGCTAGGCCCAAT 3692
 QY 969 TACGGCTCTGTGTGATGATTAAGATTTTACTGCAATTTTCCGATTCGCTTTT 1028
 DB 3693 TACGGCTCTGTGTGATGATTAAGATTTTACTGCAATTTTCCGATTCGCTTTT 3752
 QY 1029 GGGCAAAACCTTACCTCCGGTAAATATCAACTTTCCGTTTGTGACATTTGTCAAAAA 1088
 DB 3753 GGGCAAAACCTTACCTCCGGTAAATATCAACTTTCCGTTTGTGACATTTGTCAAAAA 3812
 QY 1089 CCCTGAACCTTACCTTCTGCGCGTACGCTAGCCTCCGCTTCTCTCCACATTTTCA 1148
 DB 3813 CCCTGAACCTTACCTTCTGCGCGTACGCTAGCCTCCGCTTCTCTCCACATTTTCA 3872
 QY 1149 AAGTACCCCTGTATCTCAATTAATTCATCTTCACTTGTCTCTTTGCTGTGGCCCTC 1208
 DB 3873 AAGTACCCCTGTATCTCAATTAATTCATCTTCACTTGTCTCTTTGCTGTGGCCCTC 3932
 QY 1209 TTTCACCTGCCCGCAATTCCTGTAGCGCTAGCGCACTTTGATTTATTTTCAAAAT 1268

DB 3933 TTCCAACTCCCGCCCAATTCCTGTAGCGGACGACCTTGTATTTATTTTCAAAAT 3992
 QY 1269 GTTTTCTCTCTACACACACAAAAAAGCGTTC 1301
 DB 3993 GTTTTCTCTCTACACACACAAAAAAGCGTTC 4025

RESULT 3
 ABV60941/C
 ID ABV60941 standard; cDNA; 626 BP.
 XX
 AC ABV60941;
 XX
 DT 13-SEP-2002 (First entry)
 XX
 DE Human prostate expression marker cDNA 60932.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001MO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 11585; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 626 BP; 356 A; 15 C; 41 G; 130 T; 84 other;

Query Match 3.4%; Score 44.2; DB 23; Length 626;
 Best Local Similarity 40.8%; Pred. No. 0.023; Indels 0; Gaps 0;
 Matches 139; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

QY 975 TCTGTGTCGATTTAGATTTTACTGCAATTTTTCGATTCGCTTTTGGGCA 1034
 DB 438 TTTTNTTNTTTTATTTTATTTTTCGCGGCGGNNNNCTCTTTTNTTTTATNTN 379

QY 1035 ACCCTACTCCGGTAATATCACTTTCCGTCGTGTACATTTGTCATAAACCCCTGA 1094
 Db 378 TNGTNNNTTT 319
 QY 1095 AACCCCACTTTTCGCGCGTGGCCAGCCCTCCGCTCTCTCCACATTTCCAAAGTAC 1154
 Db 318 TTTTNTT 259
 QY 1155 CCCTGATTCATCAATATCATCTTCACCTGTCGTCTTTCGTCGCGCTCTCCAA 1214
 Db 258 TTTTNTNTTATTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 199
 QY 1215 CTCGCCCAAAATTCGTACGCGTACGCGCTTGTATTTATTTTCAAAATGTTTC 1274
 Db 198 TNAATTTTNTT 139
 QY 1275 TCTCTACACACAAACAAACGCTTCAAAAAAAAAAAAA 1315
 Db 138 TNNNAAAAAAAAAAAAAAAAAANGAAAAAAAAAAAAAAAA 98

RESULT 4

AA158066
 ID AA158066 standard: cDNA: 3160 BP.

AC AA158066;

DT 22-OCT-2001 (first entry)

DE Human polynucleotide SEQ ID NO 269.

XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.

XX Homo sapiens.

PN WO200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US34263.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0596042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HXSEQ INC.

XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Dirmann RT;

DR WPI: 2001-442253/47.

DR P-PSDB: AAM38910.

XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 PS Claim 1; SEQ ID NO 269; 10078pp; English.
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAAM2213) with noctropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

SO Sequence 3160 BP; 941 A; 648 C; 665 G; 906 T; 0 other;

Query Match 3.28; Score 42; DB 22; Length 3160;
 Best Local Similarity 64.3%; Pred. No. 0.22;
 Matches 63; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1218 CCCCCAAATTCGTCGCGTACGCGCTTGTATTTATTTTCAAAATGTTTCCTC 1277

Db 2998 CCCCTTATTCGTCTTGTGAAAAAGTGAACATGTCATTTTATTAACATTTTCAT 3057

QY 1278 CTACACACACAAACAAACGCTTCAAAAAAAAAAAAA 1315

Db 3058 CAAAAAIAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3095

RESULT 5

AB052458
 ID AB052458 standard: DNA: 545 BP.

AC AB052458;

DT 12-JUL-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 39049.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.

XX Homo sapiens.

OS WO200218632-A2.

PN 07-MAR-2002.

PF 01-SEP-2001; 2001WO-EP10074.

PR 01-SEP-2000; 2000DE-1043826.

PR 05-SEP-2000; 2000DE-1044543.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Gnetig D;

DR WPI: 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA -

XX Claim 12; 56pp + Sequence listing; 56pp; German.

XX This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers

OY 1306 AAAAAAAAAA 1315
 DB 119 AAAAAAAAAA 128

RESULT 13

ABV40163
 ID ABV40163 standard; cDNA; 556 BP.
 XX
 AC ABV40163;
 XX
 DT 16-SEP-2002 (first entry)
 XX

DE Human prostate expression marker CDNA 40154.
 XX

KM Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX

PN WO200160860-A2.
 XX

PD 23-AUG-2001.
 XX

PF 20-FEB-2001; 2001WO-US05171.
 XX

PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX

PI Schlegel R, Endege WO, Monahan JE;
 XX

WPI; 2001-662795/76.
 XX

PT Novel isolated nucleic acid molecule associated with cancerous state of
 prostate cells and correlating with presence of prostate cancer, useful
 for detecting presence of prostate cancer, stage of prostate cancer -
 XX

PS Claim 1; Page 8115; 11750pp; English.
 XX

CC The invention relates to an isolated nucleic acid molecule (I) comprising
 a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC

Sequence 556 BP; 389 A; 1 C; 51 G; 113 T; 2 other;
 SQ

Query Match 3.0%; Score 39.6; DB 23; Length 556;
 Best Local Similarity 72.9%; Pred. No. 0.47; Mismatches 19; Indels 0; Gaps 0;
 Matches 51; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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 DB 59 TTTTATTTTATTTTTCGAATGTTTCCTGACACACAAACAAACGGTTCAAA 1111
 OY 1306 AAAAAAAAAA 1315
 DB 119 AAAAAAAAAA 128

DB 119 AAAAAAAAAA 128

RESULT 14

ABV42105
 ID ABV42105 standard; cDNA; 556 BP.
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 AC ABV42105;
 XX
 DT 16-SEP-2002 (first entry)
 XX

DE Human prostate expression marker CDNA 42096.
 XX

KM Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX

PN WO200160860-A2.
 XX

PD 23-AUG-2001.
 XX

PF 20-FEB-2001; 2001WO-US05171.
 XX

PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX

PI Schlegel R, Endege WO, Monahan JE;
 XX

WPI; 2001-662795/76.
 XX

PT Novel isolated nucleic acid molecule associated with cancerous state of
 prostate cells and correlating with presence of prostate cancer, useful
 for detecting presence of prostate cancer, stage of prostate cancer -
 XX

PS Claim 1; Page 8441; 11750pp; English.
 XX

CC The invention relates to an isolated nucleic acid molecule (I) comprising
 a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC

Sequence 556 BP; 389 A; 1 C; 51 G; 113 T; 2 other;
 SQ

Query Match 3.0%; Score 39.6; DB 23; Length 556;
 Best Local Similarity 72.9%; Pred. No. 0.47; Mismatches 19; Indels 0; Gaps 0;
 Matches 51; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1246 TTGATTTATTTTTCGAATGTTTCCTGACACACAAACAAACGGTTCAAA 1305
 DB 59 TTTTATTTTATTTTTCGAATGTTTCCTGACACACAAACAAACGGTTCAAA 1111
 OY 1306 AAAAAAAAAA 1315
 DB 119 AAAAAAAAAA 128

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents, NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1314.6	100.0	1315	US-09-234-186-2	Sequence 2, Appl
2	1314.6	100.0	1315	US-09-233-527-2	Sequence 2, Appl
3	1314.6	100.0	1315	PCT-US93-05651-2	Sequence 2, Appl
4	1313	99.8	1315	US-09-234-186-4	Sequence 4, Appl
5	1313	99.8	1315	US-09-234-186-5	Sequence 5, Appl
6	1313	99.8	1315	US-09-234-186-6	Sequence 6, Appl
7	1313	99.8	1315	US-09-233-527-4	Sequence 4, Appl
8	1313	99.8	1315	US-09-233-527-5	Sequence 5, Appl
9	1313	99.8	1315	US-09-233-527-6	Sequence 6, Appl
10	632.6	48.1	6559	US-09-234-186-1	Sequence 1, Appl
11	632.6	48.1	6559	US-09-234-186-1	Sequence 1, Appl
12	632.6	48.1	6559	PCT-US93-05651-1	Sequence 1, Appl
13	81.8	6.2	7218	US-08-232-463-14	Sequence 14, Appl
14	55.6	4.2	7218	US-08-232-463-14	Sequence 14, Appl
15	47.6	3.6	289	US-09-007-005-17	Sequence 17, Appl
16	47.6	3.6	289	US-09-244-796-17	Sequence 17, Appl
17	36.8	2.8	2395	US-09-149-476-159	Sequence 159, Appl
18	36.8	2.8	1299	US-09-222-938A-39	Sequence 39, Appl
19	36.4	2.8	5852	US-07-867-106-2	Sequence 17, Appl
20	35.6	2.7	289	US-09-007-005-17	Sequence 17, Appl
21	35.6	2.7	289	US-09-244-796-17	Sequence 17, Appl
22	35.4	2.7	1307	US-09-250-609-3	Sequence 3, Appl
23	35	2.7	248	US-09-007-005-32	Sequence 32, Appl
24	35	2.7	248	US-09-244-796-32	Sequence 32, Appl
25	35	2.7	277	US-09-007-005-3	Sequence 3, Appl
26	35	2.7	277	US-09-244-796-3	Sequence 3, Appl
27	34.8	2.6	1033	US-09-173-300-46	Sequence 46, Appl

28	34.8	2.6	3073	US-07-688-352C-31	Sequence 31, Appl
29	34.8	2.6	3073	US-08-474-379C-31	Sequence 31, Appl
30	34.8	2.6	3073	US-09-146-249A-31	Sequence 31, Appl
31	34.8	2.6	3073	US-08-206-188B-31	Sequence 31, Appl
32	34.8	2.6	3073	PCT-US91-02714-30	Sequence 30, Appl
33	34.4	2.6	3157	5198347-3	Patent No. 5198347
34	34.2	2.6	611	US-09-385-982-393	Sequence 393, App
35	33.8	2.6	882	US-08-909-965C-9	Sequence 9, Appl
36	33.8	2.6	1889	US-09-187-050-1	Sequence 1, Appl
37	33.4	2.5	1096	US-09-461-697-26	Sequence 26, Appl
38	33.4	2.5	2791	US-09-570-367C-1	Sequence 1, Appl
39	33.2	2.5	1313	US-08-149-476-112	Sequence 112, App
40	33.2	2.5	2007	US-08-747-221B-36	Sequence 36, Appl
41	33.2	2.5	2007	US-08-747-221B-36	Sequence 36, Appl
42	33.2	2.5	2007	US-09-005-051-36	Sequence 38, Appl
43	33.2	2.5	2007	US-09-005-051-36	Sequence 38, Appl
44	33	2.5	1466	US-08-984-919A-10	Sequence 10, Appl
45	33	2.5	1466	US-08-984-919A-12	Sequence 12, Appl

ALIGNMENTS

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RESULT 1
US-09-234-186-2
; Sequence 2, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; EARLIER FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ. ID NOS.: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-234-186-2

Query Match      100.0%   Score 1314.6;   DB 4;   Length 1315;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 1315;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY 1 TTGGAATGACACGCTGCACAGGCGGCAACTCGCTGACGATCCGGCGTATCGCGAGCA 60
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QY 61 ACGATGGCGACGCGGAGATGGAAGAGTTTCGGGATTAAGGCGACAGCCCAACCAT 120
    |||||||
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    |||||||

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    |||||||
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QY 181 AGAATTCATGGAGAGTCATTTGATGAAATCAATGATGGAGAGCCCAAGCCTT 240
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Db 181 AGAATGTCATCGAGAGTCATTTGATGGAATAATCATGATTGGAGAGCCAGGCTT 240
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Db 241 GATATGAGGAGATTTTGGTCGACATTTTCACGACCGAATCCGGGAAACGGAATGGA 300
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Db 301 TGGTTGGAGACCGGAGATTCCGCTGTGAGTCAACCGGAGCAGCAAAATGATGCACTT 360
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Db 361 ATGGGAACGATTTTCGGAAGAAGACCGGGAATTTTGGAGACTTCTGTGACAGCTG 420
QY 421 CTGCACTGCCCAGAAATCTCATTTTCACTGTATCAGAGTGTGTCGAGCGTTGGAAT 480
Db 421 CTGCACTGCCCAGAAATCTCATTTTCACTGTATCAGAGTGTGTCGAGCGTTGGAAT 480
QY 481 GCACAGACAGATCATATCCAAATGCTTATGAGACGTTTATGAGTCTTATCTGTCGCG 540
Db 481 GCACAGACAGATCATATCCAAATGCTTATGAGACGTTTATGAGTCTTATCTGTCGCG 540
QY 541 GGTTCGATGTCGCAAAATATGATGATCCGTGGAACCTGAGGAGCAAGTGCAGAACTTC 600
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RESULT 2
US-09-233-527-2
Sequence 2, Application US/09233527
Patent No. 6465617
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
INVENTOR: Horvitz, H. Robert
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
FILE REFERENCE: 0197/201004
CURRENT APPLICATION NUMBER: US/09/233,527
PRIOR APPLICATION NUMBER: 07/998,933
PRIOR FILING DATE: 1992-06-12
PRIOR APPLICATION NUMBER: 07/927,681
PRIOR FILING DATE: 1992-08-10
PRIOR APPLICATION NUMBER: 08/288,295
PRIOR FILING DATE: 1994-08-10
PRIOR APPLICATION NUMBER: 08/801,248
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1315
TYPE: DNA
ORGANISM: Caenorhabditis elegans
FEATURE:
NAME/KEY: CDS
LOCATION: (7)...(846)
US-09-233-527-2
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 241 GATATGAGGAGATTTTGGTCGACATTTTCACGACCGAATCCGGGAAACGGAATGGA 300
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Db 781 GTAACAGCTGGAGCCATTGGAATCGTTGAGTCGTGTGTGGCGGATGATGTTGACG 840
QY 841 TTGAAGTAACTGATTCATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Db 841 TTGAAGTAACTGATTCATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
QY 901 ATCTCAATTTTTCCTCAGTATTCCTCATCTTTCATCTTGAAGTGAAGAGTGGAAAGCTAG 960
Db 901 ATCTCAATTTTTCCTCAGTATTCCTCATCTTTCATCTTGAAGTGAAGAGTGGAAAGCTAG 960
QY 961 CCACAAATTAAGGCTCTCTGTGTGATTAACGATTTTACGCAATTTTTCGATTCGCT 1020
Db 961 CCACAAATTAAGGCTCTCTGTGTGATTAACGATTTTACGCAATTTTTCGATTCGCT 1020
QY 1021 TTTTTCCTGCGCAACCTCTCTGCGTAAATCAACTTTCGCGTGTGATTAATTC 1080
Db 1021 TTTTTCCTGCGCAACCTCTCTGCGTAAATCAACTTTCGCGTGTGATTAATTC 1080
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Db 1081 GTCAAAAACCTGAAACCTTAATTTTTCGCGTGTGATTAATTC 1140
QY 1141 CATTTCCAAAGTACCTCTGATCTCAATTAATTAATTAATTAATTAATTAATTAAT 1200
Db 1141 CATTTCCAAAGTACCTCTGATCTCAATTAATTAATTAATTAATTAATTAATTAAT 1200
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Db 1201 GTGSCCTCTTCCAACTCCCGCAAAATCTGTAAGGCTAGCGGCTTGTATTAATTTT 1260
QY 1261 TTCAAATTTGTTCTCTCTACAAACAAAAAAGGTTCAAAAAA 1315
Db 1261 TTCAAATTTGTTCTCTCTACAAACAAAAAAGGTTCAAAAAA 1315

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; LOCATION: 7..846
; OTHER INFORMATION: /product= "Ced-9"
PCT-US93-05651-2
Query Match 100.0%; Score 1314.6; DB 5; Length 1315;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGACATGACAGCTGCGACGGCGGACAACTGCTGACGAATCCGCGTATCGGCGACA 60
Db 1 TTTGACATGACAGCTGCGACGGCGGACAACTGCTGACGAATCCGCGTATCGGCGACA 60
QY 61 ACATGCGCAGCTGGAGAGTGAAGAGTTCGCGGATTAAGGACAGAGCCGCGAT 120
Db 61 ACATGCGCAGCTGGAGAGTGAAGAGTTCGCGGATTAAGGACAGAGCCGCGAT 120
QY 121 TTTGAATCAATTAATGATCTGAGACTTTCACGCAACCGAATCCGCAAAACGGAATGGA 180
Db 121 TTTGAATCAATTAATGATCTGAGACTTTCACGCAACCGAATCCGCAAAACGGAATGGA 180
QY 181 AGAATGTCATGGAGAGTCAATTTGATGAAAAATCAATGATTTGGAAAGACCAAGCTT 240
Db 181 AGAATGTCATGGAGAGTCAATTTGATGAAAAATCAATGATTTGGAAAGACCAAGCTT 240
QY 241 GATATCGAGGATTTGTGTGCACTATTTACGCAACCGAATCCGCAAAACGGAATGGA 300
Db 241 GATATCGAGGATTTGTGTGCACTATTTACGCAACCGAATCCGCAAAACGGAATGGA 300
QY 301 TGGTTTGAAGACCGGGATTTGCGTGTGAGTGAACCGGACACGGAATGAGAGCTT 360
Db 301 TGGTTTGAAGACCGGGATTTGCGTGTGAGTGAACCGGACACGGAATGAGAGCTT 360
QY 361 ATGGAGACGATTTGTGAGAGAGAGACAGCGGGAATTTTGAACCTTCTGTGAGAGCTG 420
Db 361 ATGGAGACGATTTGTGAGAGAGAGACAGCGGGAATTTTGAACCTTCTGTGAGAGCTG 420
QY 421 CTCGAGTCCCGAATTCATTTTACGATATGATGATGATGATGATGATGATGATGAT 480
Db 421 CTCGAGTCCCGAATTCATTTTACGATATGATGATGATGATGATGATGATGATGAT 480
QY 481 GCACAGACAGATCAATGTCGAATGTCGAATGTCGAATGTCGAATGTCGAATGTCGAAT 540
Db 481 GCACAGACAGATCAATGTCGAATGTCGAATGTCGAATGTCGAATGTCGAATGTCGAAT 540
QY 541 GGTTCGTAGCTGCAAAAATATGTAATCCGTGAACTGAGGAGCAAGTCCGAACCTC 600
Db 541 GGTTCGTAGCTGCAAAAATATGTAATCCGTGAACTGAGGAGCAAGTCCGAACCTC 600
QY 601 TTCGTTACACATCGCTGTTCATCAAAAACGGGATCCGCAACAACATGGAAGAACACAT 660
Db 601 TTCGTTACACATCGCTGTTCATCAAAAACGGGATCCGCAACAACATGGAAGAACACAT 660
QY 661 CGGAGCTGGAGCGACTTCATGACACTGCGAAACAAATGAAAGAGACTCGAACGACGA 720
Db 661 CGGAGCTGGAGCGACTTCATGACACTGCGAAACAAATGAAAGAGACTCGAACGACGA 720
QY 721 GAACTGAAAAAGTGGAGCGCGGAGACAGAACAGAGCGTGTGATGATGGCGCTGA 780
Db 721 GAACTGAAAAAGTGGAGCGCGGAGACAGAACAGAGCGTGTGATGATGGCGCTGA 780
QY 781 GTAACAGCTGGAGCCATTGGAATCGTTGAGTCGTGTGTGGCGGATGATGTTGACG 840
Db 781 GTAACAGCTGGAGCCATTGGAATCGTTGAGTCGTGTGTGGCGGATGATGTTGACG 840
QY 841 TTGAAGTAACTGATTCATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Db 841 TTGAAGTAACTGATTCATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
QY 901 ATCTCAATTTTTCCTCAGTATTCCTCATCTTTCATCTTGAAGTGAAGAGTGGAAAGCTAG 960
Db 901 ATCTCAATTTTTCCTCAGTATTCCTCATCTTTCATCTTGAAGTGAAGAGTGGAAAGCTAG 960
QY 961 CCACAAATTAAGGCTCTCTGTGTGATTAACGATTTTACGCAATTTTTCGATTCGCT 1020

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RESULT 3
PCT-US93-05651-2
Sequence 2, Application PC/TUS9305651

GENERAL INFORMATION:
TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05651
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1315 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS

|||||
Db 961 CCACAAATTAGGCTCTGTGTGATTTAGATTTTACTCAATTTTTCOCGATTCGCT 1020
Qy 1021 TTTTGTGGCAAAACCTACTTCCGTAATATCAATTTCCGTGCTGATTC 1080
Db 1021 TTTTGTGGCAAAACCTACTTCCGTAATATCAATTTTCCGTGCTGATTC 1080
Qy 1081 GTCAAAAACCTGAAACCTACTTCTCGCGGTGCGCTACCCCTCTCTTCCA 1140
Db 1081 GTCAAAAACCTGAAACCTACTTCTCGCGGTGCGCTACCCCTCTCTTCCA 1140
Qy 1141 CATTTCCAAAGTACCCCTGATCTCAATATTCATCTTCACTTACTGCTCTTTTGT 1200
Db 1141 CATTTCCAAAGTACCCCTGATCTCAATATTCATCTTCACTTACTGCTCTTTTGT 1200
Qy 1201 GTGGCCTCTTCCAACTCCCGCAAAATTCCTGTACCGCGATCGCTTGTATTTT 1260
Db 1201 GTGGCCTCTTCCAACTCCCGCAAAATTCCTGTACCGCGATCGCTTGTATTTT 1260
Qy 1261 TTCAATTTGTTTCTCTCTACACACAAAAAAGGTTCAAAAAA 1315
Db 1261 TTCAATTTGTTTCTCTCTCTACACACAAAAAAGGTTCAAAAAA 1315

RESULT 4
US-09-234-186-4
: Sequence 4, Application US/09234186
: Patent No. 6312947
: GENERAL INFORMATION:
: APPLICANT: Horvitz, R. Robert
: APPLICANT: Hengartner, Michael
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
: TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: 01997/201005
: CURRENT APPLICATION NUMBER: US/09/234,186
: EARLIER FILING DATE: 1999-01-20
: EARLIER APPLICATION NUMBER: 07/898,933
: EARLIER FILING DATE: 1992-06-12
: EARLIER APPLICATION NUMBER: 07/927,681
: EARLIER FILING DATE: 1992-08-10
: EARLIER APPLICATION NUMBER: 08/288,295
: EARLIER FILING DATE: 1994-08-10
: EARLIER APPLICATION NUMBER: 08/801,248
: EARLIER FILING DATE: 1997-02-19
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 1315
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (7)...(846)
US-09-234-186-4

Query Match 99.8%; Score 1313; DB 4; Length 1315;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 181 AGAATGTCATCGAGAGTCAATTTGATGAAAAATCAATTTGGAGAGCAAGGCTT 240
Qy 241 GATATGAGGAGATTGTGGTCGACTATTTACAGCAACCGAATCCGGCAAAAGCAATGGA 300
Db 241 GATATGAGGAGATTGTGGTCGACTATTTACAGCAACCGAATCCGGCAAAAGCAATGGA 300
Qy 301 TGGTTTGAGACACCGGAGATTGGCGTGTGAGTGAACCGGACACGAAATGATGCGAGTT 360
Db 301 TGGTTTGAGACACCGGAGATTGGCGTGTGAGTGAACCGGACACGAAATGATGCGAGTT 360
Qy 361 ATGGGAACGATATTCAGAGAAGACACCGGAAATTTTGAACCTTCTGTAGACGCTG 420
Db 361 ATGGGAACGATATTCAGAGAAGACACCGGAAATTTTGAACCTTCTGTAGACGCTG 420
Qy 421 CTGCGAGTGGCCAGATTCATTTTCTACTGTATTCAGATGTTGGTTCGAGGTTGGAAT 480
Db 421 CTGCGAGTGGCCAGATTCATTTTCTACTGTATTCAGATGTTGGTTCGAGGTTGGAAT 480
Qy 481 GCACAGACAGATCAATGTCCAATGTCATATGAGACGTTTGTATGATGATCTGTTGGGC 540
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Qy 541 GGTTCGTAGCTGCAAAAATGATGATCCGTGGAATCTGACGAGACAGTGGAAACCTC 600
Db 541 GGTTCGTAGCTGCAAAAATGATGATCCGTGGAATCTGACGAGACAGTGGAAACCTC 600
Qy 601 TTGCTTTACACATCGCTGTTCATCAAAACGCGGATCCGCAACACTGGAGAGACACAT 660
Db 601 TTGCTTTACACATCGCTGTTCATCAAAACGCGGATCCGCAACACTGGAGAGACACAT 660
Qy 661 CGAGCTGGGAGACTTCATGACACTCGGAAAAAACAATGAAGAGACTACGACAGAGCA 720
Db 661 CGAGCTGGGAGACTTCATGACACTCGGAAAAAACAATGAAGAGACTACGACAGAGCA 720
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Db 781 GTTACAGCTGGAGCCATTTGGAATCGTTGAGTGTGTGTTGGGGGATGATGTTTACG 840
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Db 841 TTGAAGTAAAGTATTCATTTGTATTAATTAATTTATGTAACAATCTTACATTTGA 900
Qy 901 ATCTCATTTTGGCTCACTGATTTCTCATCTTTGAATGGAAGAGTGGAAAGCTAGG 960
Db 901 ATCTCATTTTGGCTCACTGATTTCTCATCTTTGAATGGAAGAGTGGAAAGCTAGG 960
Qy 961 CCACAAATTAGGCTCTGTGTGATTTAGATTTTACTGCAATTTTTCGATTCGCT 1020
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Qy 1141 CATTTCCAAAGTACCCCTGATCTCAATATTCATCTTCACTTACTGCTCTTTTGT 1200
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Db 1261 TTCAAATTTCTCTCTCTACACACACAAAAAAGGTTCAAAAAA 1315

RESULT 5
US-09-234-186-5
; Sequence 5, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-234-186-5

Query Match 99.8%; Score 1313; DB 4; Length 1315;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTTGGAGACAGCGTGTGAGCGGACACACCTGTCGAGTATCGGGGTACGGCGACGA 60
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Qy 61 ACGATGCGAGCTGGCGAGATGAAGAGTTTCTGGGGATMAAAGGCACAGACCCGAT 120
Db 61 ACGATGCGAGCTGGCGAGATGAAGAGTTTCTGGGGATMAAAGGCACAGACCCGAT 120

Qy 121 TTTGGAATCATAGTGTGAGTCTGAGACTTCCATCACCAGTATAGGCGAGCTTCAACGCA 180
Db 121 TTTGGAATCATAGTGTGAGTCTGAGACTTCCATCACCAGTATAGGCGAGCTTCAACGCA 180

Qy 181 AGAATGTCATCGAGAGATGATGATGAAAAATCAATGATGGAAGACCAAGGCTT 240
Db 181 AGAATGTCATCGAGAGATGATGATGAAAAATCAATGATGGAAGACCAAGGCTT 240

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Db 241 GATATCGAGGATTTGTGGTCACTATTTCACGACCGAATCCGCAAAACGGAATGGAA 300

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Qy 361 ATGGAGAGATTTGAGACAGACCGGAAATTTTGGAGCTTGTGAGCAGCTG 420
Db 361 ATGGAGAGATTTGAGACAGACCGGAAATTTTGGAGCTTGTGAGCAGCTG 420

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Db 901 ATCTCAATTTTCTGCTCACTATCTCATCTTTGAACTGGAAGAGTGGAAACCTAGG 960

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Qy 1081 GTCAAAATCCCTGAACCTTAATTTCTGCGCGCTAGCGCTCCGCTCTCTTCCA 1140
Db 1081 GTCAAAATCCCTGAACCTTAATTTCTGCGCGCTAGCGCTCCGCTCTCTTCCA 1140

Qy 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAAT 1200
Db 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAAT 1200

Qy 1201 GTGGCCTCTTCAACCTCCCGCAAAATCCGTGACGCTAGCGCACTTGTATTTATTTT 1260
Db 1201 GTGGCCTCTTCAACCTCCCGCAAAATCCGTGACGCTAGCGCACTTGTATTTATTTT 1260

Qy 1261 TTCAAATTTCTCTCTCTACACACAAAAAAGGTTCAAAAAA 1315
Db 1261 TTCAAATTTCTCTCTCTACACACAAAAAAGGTTCAAAAAA 1315

RESULT 6
US-09-234-186-6
; Sequence 6, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295

; EARLIER FILING DATE: 1994-08-10
 ; EARLIER APPLICATION NUMBER: 08/801,248
 ; EARLIER FILING DATE: 1997-02-19
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 1315
 ; TYPE: DNA
 ; ORGANISM: Caenorhabditis elegans
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)...(846)
 US-09-234-186-6

Query Match 99.8%; Score 1313; DB 4; Length 1315;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTGAGATGACACGCTGACGCGGACAACTCGTGACGAATCCGGCGTATCGGCGACGA 60
 Db 1 TTTGAGATGACACGCTGACGCGGACAACTCGTGACGAATCCGGCGTATCGGCGACGA 60
 QY 61 ACGATGGCGACTGCGGAGATGAGAGATTTCTGGGAGATAAAAGCACAGACCCACCGAT 120
 Db 61 ACGATGGCGACTGCGGAGATGAGAGATTTCTGGGAGATAAAAGCACAGACCCACCGAT 120
 QY 121 TTTGAGATCAATAGTATGATGCTCAGACTTGGCATTACCGAGTAGGCAAGGCTTCGACGGGA 180
 Db 121 TTTGAGATCAATAGTATGATGCTCAGACTTGGCATTACCGAGTAGGCAAGGCTTCGACGGGA 180
 QY 181 AGAATGTCATCGGAGACTCAATTGATGGAATAATCAATGATTTGGAGAGACCAAGGCTT 240
 Db 181 AGAATGTCATCGGAGACTCAATTGATGGAATAATCAATGATTTGGAGAGACCAAGGCTT 240
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 Db 241 GATATCGAGGGAGTTGTGTGACTATTTCACGACCGAATCCGGCAAAAGGGAATGGAA 300
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 Db 301 TGGTTTGAGACACCGGAGATTCGCGTGTGAGTGCACCGGAGACGAATGATCGAGTT 360
 QY 361 ATGGGAACGATTTTCGAGAAACAGACCGGAAATTTTGAGACCTTGTGAGACACTG 420
 Db 361 ATGGGAACGATTTTCGAGAAACAGACCGGAAATTTTGAGACCTTGTGAGACACTG 420
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 Db 421 CTGCGAGTGGCCAGATCTCAATTTTCACTGATACAGATGCGTTGCGAGCGTTGGAAT 480
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 Db 481 GCACAGACAGATCAATGTCATATGCTTATGAGAGTGTGATAGTCTTAATCTCGTTCGCG 540
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 Db 601 TTGCTTTACATCGCTGTGCTTCAAAAACGGGATCCGCAACACTGGAAGGAGACACAT 660
 QY 661 CGGAGCTGGGACGACTTCATGACACTCGGAAACAAATGAAAGAGGACTACGAACGAGCA 720
 Db 661 CGGAGCTGGGACGACTTCATGACACTCGGAAACAAATGAAAGAGGACTACGAACGAGCA 720
 QY 721 GAACCTGAAAAAGTGGGACCGCGGAGACGAGAACGAGCGTGTGATGATTTGGGCGCTGGA 780
 Db 721 GAACCTGAAAAAGTGGGACCGCGGAGACGAGAACGAGCGTGTGATGATTTGGGCGCTGGA 780
 QY 781 GTAAACAGCTGAGCCATTGGAATGTTGGAATCTGCTGTGTGTGGGCGGATGATTTGAGC 840
 Db 781 GTAAACAGCTGAGCCATTGGAATGTTGGAATCTGCTGTGTGTGGGCGGATGATTTGAGC 840

QY 841 TTGAGTAACGTAATTCATTTGTAATAATTAATTAATTTACACACGCTTACATTGA 900
 Db 841 TTGAGTAACGTAATTCATTTGTAATAATTAATTAATTTGTAACACGCTTACATTGA 900
 QY 901 ATCTCAATTTTGGCTACGATGATCTCTCAATCCCTTGAAGTGAAGAGTGGAAAGCTAGG 960
 Db 901 ATCTCAATTTTGGCTACGATGATCTCTCAATCCCTTGAAGTGAAGAGTGGAAAGCTAGG 960
 QY 961 CCACAAATTTAGGCTCTCTGTGTGATTTACGATTTTACTGCAATTTTCCGATTCCT 1020
 Db 961 CCACAAATTTAGGCTCTCTGTGTGATTTACGATTTTACTGCAATTTTCCGATTCCT 1020
 QY 1021 TTTTGTGGCCAAACCCGTAATTCGCGGTAATTCGCACTTTCCGCTCTGTACATTTC 1080
 Db 1021 TTTTGTGGCCAAACCCGTAATTCGCGGTAATTCGCACTTTCCGCTCTGTACATTTC 1080
 QY 1081 GTCAAAAACCCGTAACCCGTAATTTTCGCGGCTAGCGCTCCGCTCTGTCA 1140
 Db 1081 GTCAAAAACCCGTAACCCGTAATTTTCGCGGCTAGCGCTCCGCTCTGTCA 1140
 QY 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTCATTTTCACTTTAAGTCTCTTTTGGT 1200
 Db 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTCATTTTCACTTTAAGTCTCTTTTGGT 1200
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 Db 1201 GTGGCCCTTCCAAACGCTCCGCAATTCGTAACGCGTACGCGGAGCTTTGATTTATTTT 1260
 QY 1261 TTCAAATTTGTTTCTCTCTACAAACAAACAAACGTTTCAAAAAAAAAAAAAA 1315
 Db 1261 TTCAAATTTGTTTCTCTCTACAAACAAACAAACGTTTCAAAAAAAAAAAAAA 1315

RESULT 7
 US-09-233-527-4
 ; Sequence 4, Application US/09233527
 ; Patent No. 6465617
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, H. Robert
 ; APPLICANT: Hengartner, Michael
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
 ; FILE REFERENCE: 01997/201004
 ; CURRENT APPLICATION NUMBER: US/09/233,527
 ; PRIOR FILING DATE: 1999-01-20
 ; PRIOR APPLICATION NUMBER: 07/896,933
 ; PRIOR FILING DATE: 1992-06-12
 ; PRIOR APPLICATION NUMBER: 07/927,681
 ; PRIOR FILING DATE: 1992-08-10
 ; PRIOR APPLICATION NUMBER: 08/288,295
 ; PRIOR FILING DATE: 1994-08-10
 ; PRIOR APPLICATION NUMBER: 08/801,248
 ; PRIOR FILING DATE: 1997-02-19
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 1315
 ; TYPE: DNA
 ; ORGANISM: Caenorhabditis elegans
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)...(846)
 US-09-233-527-4

Query Match 99.8%; Score 1313; DB 4; Length 1315;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTGAGATGACACGCTGACGCGGACAACTCGTGACGAATCCGGCGTATCGGCGACGA 60
 Db 1 TTTGAGATGACACGCTGACGCGGACAACTCGTGACGAATCCGGCGTATCGGCGACGA 60

QY 61 ACGATGCGACTGGCGAGATGAAGAGTTCCTGGGATATAAAGGACAGAGCCACCGAT 120
 DB 61 ACGATGCGACTGGCGAGATGAAGAGTTCCTGGGATATAAAGGACAGAGCCACCGAT 120
 QY 121 TTGGGAATCAATAGTAGTGTCTCAGAGACTTCCCATCACCGAGTAGAGCGCTTGACGCGA 180
 DB 121 TTGGGAATCAATAGTAGTGTCTCAGAGACTTCCCATCACCGAGTAGAGCGCTTGACGCGA 180
 QY 181 AGAATGTCATCGAGAGTCAATGATGGAATAATCAATATTTGGGAAGGCCAAGCTT 240
 DB 181 AGAATGTCATCGAGAGTCAATGATGGAATAATCAATATTTGGGAAGGCCAAGCTT 240
 QY 241 GATATCGAGGATTTGTGTGCTGACTATTTCACGACCGAATCCGGCAAAACGGAATGAA 300
 DB 241 GATATCGAGGATTTGTGTGCTGACTATTTCACGACCGAATCCGGCAAAACGGAATGAA 300
 QY 301 TGGTTTGGAGACCGGGATTTGCGGTGTGAGTGCACCGGAGCAGCAAGATGCGAGTT 360
 DB 301 TGGTTTGGAGACCGGGATTTGCGGTGTGAGTGCACCGGAGCAGCAAGATGCGAGTT 360
 QY 361 ATGGGAACGATTTTCGAGAAGACAGCGGGAATTTTGAACCTTCTGTGACAGCTT 420
 DB 361 ATGGGAACGATTTTCGAGAAGACAGCGGGAATTTTGAACCTTCTGTGACAGCTT 420
 QY 421 CTCGACGTGCCAGAAATCTCATTTTCTACTGATCAGAGATGCTTGGAGCGTTGGAAT 480
 DB 421 CTCGACGTGCCAGAAATCTCATTTTCTACTGATCAGAGATGCTTGGAGCGTTGGAAT 480
 QY 481 GCACAGACAGATCAATGCTCAATGTCTTATGAGCGTTTGAAGGTCTAATCTGCTGCG 540
 DB 481 GCACAGACAGATCAATGCTCAATGTCTTATGAGCGTTTGAAGGTCTAATCTGCTGCG 540
 QY 541 GGTTCGTAGCTGCAAAATGATGGAATCCGTGGAATCGAGGACAAAGTCCAAACCTC 600
 DB 541 GGTTCGTAGCTGCAAAATGATGGAATCCGTGGAATCGAGGACAAAGTCCAAACCTC 600
 QY 601 TTGCTTACACATCGCTGTTCATCAAAACCGGATCCGCAACATGGAAGAACACAT 660
 DB 601 TTGCTTACACATCGCTGTTCATCAAAACCGGATCCGCAACATGGAAGAACACAT 660
 QY 661 CGGAGCTGGAGCAGACTTCATGACACTCGGAAAAAATGAAGAGGACTGAGAGAGCA 720
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 DB 721 GAAGCTGAAAAAGTGGGAGCGCGGAAGCAGAACGAGTGTGATGATTTGGCGCTGGA 780
 QY 781 GTAAAGCTGAGGACATTTGAATCTGTGAGTGTGTGAGGAGATGATTCAGC 840
 DB 781 GTAAAGCTGAGGACATTTGAATCTGTGAGTGTGTGAGGAGATGATTCAGC 840
 QY 841 TTGAAGTAAAGTAAATTTGTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
 DB 841 TTGAAGTAAAGTAAATTTGTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
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 DB 901 ATTCATTTTGTCTCATGATTTCTCTCATCTTGAACCTGGAAGAGTGGAAAGCTAG 960
 QY 961 CCACAATTTAGGCTCTCTGTGCTGATTTTACTGCAATTTTTCGATTTGCTT 1020
 DB 961 CCACAATTTAGGCTCTCTGTGCTGATTTTACTGCAATTTTTCGATTTGCTT 1020
 QY 1021 TTTTGTGCGCAAAACCTTCTCCGGTAATATCAACTTTTCCGTTCTGTACATTTTC 1080
 DB 1021 TTTTGTGCGCAAAACCTTCTCCGGTAATATCAACTTTTCCGTTCTGTACATTTTC 1080
 QY 1081 GTCAAAAACCTGAAACCTTAATTTTCTGCGGCTAGGCTCCCGCTCTCTTCCA 1140
 DB 1081 GTCAAAAACCTGAAACCTTAATTTTCTGCGGCTAGGCTCCCGCTCTCTTCCA 1140

QY 1141 CATTTCAAAAGTACCCTGTATCTCAATTAATTCATCTTCACTTAACTGTCTTTTGT 1200
 DB 1141 CATTTCAAAAGTACCCTGTATCTCAATTAATTCATCTTCACTTAACTGTCTTTTGT 1200
 QY 1201 GTGGCCTTTCACACTCCCCCAAAATTCCTGTAGCGTAGCGGACTTGTATTATTTT 1260
 DB 1201 GTGGCCTTTCACACTCCCCCAAAATTCCTGTAGCGTAGCGGACTTGTATTATTTT 1260
 QY 1261 TTCAAAATGTTTCTCTCTACACAACAAAAAACGGTTCAAAAAATTTTTTTTTT 1315
 DB 1261 TTCAAAATGTTTCTCTCTACACAACAAAAAACGGTTCAAAAAATTTTTTTTTT 1315

RESULT 8
 US-09-233-527-5
 ; Sequence 5, Application US/09233527
 ; Patent No. 6465617
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, H. Robert
 ; APPLICANT: Hengartner, Michael
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
 ; FILE REFERENCE: 0197/201004
 ; CURRENT APPLICATION NUMBER: US/09/233,527
 ; PRIOR FILING DATE: 1999-01-20
 ; PRIOR APPLICATION NUMBER: 07/898,933
 ; PRIOR FILING DATE: 1992-06-12
 ; PRIOR APPLICATION NUMBER: 07/927,681
 ; PRIOR FILING DATE: 1992-08-10
 ; PRIOR APPLICATION NUMBER: 08/288,295
 ; PRIOR FILING DATE: 1994-08-10
 ; PRIOR APPLICATION NUMBER: 08/801,248
 ; PRIOR FILING DATE: 1997-02-19
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 1315
 ; TYPE: DNA
 ; ORGANISM: Caenorhabditis elegans
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)...(846)
 ; US-09-233-527-5

Query Match 99.8%; Score 1313; DB 4; Length 1315;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGTACACGCTGCGACGGCGGACACAACCTGAGCAATTCGGGCTATCGGCGACGA 60
 DB 1 TTGGAGTACACGCTGCGACGGCGGACACAACCTGAGCAATTCGGGCTATCGGCGACGA 60
 QY 61 ACGATGCGACTGGCGAGATGAAGAGTTCCTGGGATATAAAGGACAGAGCCACCGAT 120
 DB 61 ACGATGCGACTGGCGAGATGAAGAGTTCCTGGGATATAAAGGACAGAGCCACCGAT 120
 QY 121 TTGGGAATCAATAGTAGTGTCTCAGAGACTTCCCATCACCGAGTAGAGCGCTTGACGCGA 180
 DB 121 TTGGGAATCAATAGTAGTGTCTCAGAGACTTCCCATCACCGAGTAGAGCGCTTGACGCGA 180
 QY 181 ACAAATGTCATCGGAGAGTCAATGATGGAATAATCAATATTTGGGAAGGCCAAGCTT 240
 DB 181 ACAAATGTCATCGGAGAGTCAATGATGGAATAATCAATATTTGGGAAGGCCAAGCTT 240
 QY 241 GATATCGAGGATTTGTGTGCTGACTATTTCACGACCGAATCCGGCAAAACGGAATGAA 300
 DB 241 GATATCGAGGATTTGTGTGCTGACTATTTCACGACCGAATCCGGCAAAACGGAATGAA 300
 QY 301 TGGTTTGGAGACCGGGATTTGCGGTGTGAGTGCACCGGAGCAGCAAGATGCGAGTT 360
 DB 301 TGGTTTGGAGACCGGGATTTGCGGTGTGAGTGCACCGGAGCAGCAAGATGCGAGTT 360

361 ATGGAGCATATTCGAGAGACGCGGAAATTTTGACCTTCGTGACAGCTG 420
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361 ATGGAGCATATTCGAGAGACGCGGAAATTTTGACCTTCGTGACAGCTG 420
421 CTCGACGTGCGGAGATTCATTTTCTACGTATCAGATGTTGGAGCGTTGAAAT 480
|||||
421 CTCGACGTGCGGAGATTCATTTTCTACGTATCAGATGTTGGAGCGTTGAAAT 480
481 GCACAGACAGATCATATGTCCTATGATGAGCTTTGATAGGCTATCTGCTGGC 540
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481 GCATAGACAGATCATATGTCCTATGATGAGCTTTGATAGGCTATCTGCTGGC 540
541 GGTTCGTAGCTGCAAAATGATGATCCGTGAACTGCAAGGCAAGTCCGAAACCTC 600
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601 TTGCTTACACATCGCTGTTTCATCAAAACGCGGATCCGCAACACTGGAAGAACACAT 660
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601 TTGCTTACACATCGCTGTTTCATCAAAACGCGGATCCGCAACACTGGAAGAACACAT 660
661 CGGAGCTGGAGACTTCATGACATCGGAAACAAATGAAAGGAGACTAGGAAGAGCA 720
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721 GAAGCTGAAAAAGTGGAGCGCGGAGAGCAAGACGAGTGGATGATGGCGCTGGA 780
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781 GTACAGCTGGAGCTTGGAAATCGTGGAGTCTGCTGGTGGCGGATGATGTTGACG 840
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781 GTACAGCTGGAGCTTGGAAATCGTGGAGTCTGCTGGTGGCGGATGATGTTGACG 840
841 TTGAAGTAACTGATTCATTTTGTAAATTAATTTATGATGACAACTCCCTACATTTGA 900
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841 TTGAAGTAACTGATTCATTTTGTAAATTAATTTATGATGACAACTCCCTACATTTGA 900
881 TTGAAGTAACTGATTCATTTTGTAAATTAATTTATGATGACAACTCCCTACATTTGA 900
901 ATCTCATTTTTCGCTACTGATTCCTCATCTTTGAACTGGAAGAGTGGAAAGCTAGG 960
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901 ATCTCATTTTTCGCTACTGATTCCTCATCTTTGAACTGGAAGAGTGGAAAGCTAGG 960
961 CCACAAATTAAGGCTCTGTGTGATTTAGATTTTACTGCAATTTTTCGATTTGCT 1020
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961 CCACAAATTAAGGCTCTGTGTGATTTAGATTTTACTGCAATTTTTCGATTTGCT 1020
1021 TTTTGTGGCCAAACCTTACCTGCGCTAATATCACTTTTCCGTTCTGTATTC 1080
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1021 TTTTGTGGCCAAACCTTACCTGCGCTAATATCACTTTTCCGTTCTGTATTC 1080
1081 GTCAAAACCTTGAACCTTATCTGCGCTGAGCTCCGCTTCCTCTTCA 1140
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1141 CATTTCCAAAGTACCTGTATCTCAATATTCATCTTCACTTAACTCTCTTTTCT 1200
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1201 GTGGCTCTTCCAACTCCGCAATTCCTGTAGCGCTAGCGAGCTTTGTATTTT 1260
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1261 TTCAATATGTTTCTCTCTACAAACAAAAAGGTTCAAAAAA 1315

RESULT 9

US-09-233-527-6
; Sequence 6, Application US/09233527

; Patent No. 6465617

; GENERAL INFORMATION:

; APPLICANT: Horvitz, H. Robert

; APPLICANT: Hengartner, Michael

; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A

;; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
;; TITLE OF INVENTION: USES THEREFOR
;; FILE REFERENCE: 01997/201004
;; CURRENT APPLICATION NUMBER: US/09/233,527
;; CURRENT FILING DATE: 1999-01-20
;; PRIOR APPLICATION NUMBER: 07/988,933
;; PRIOR FILING DATE: 1992-06-12
;; PRIOR APPLICATION NUMBER: 07/927,681
;; PRIOR FILING DATE: 1992-08-10
;; PRIOR APPLICATION NUMBER: 08/288,295
;; PRIOR FILING DATE: 1994-08-10
;; PRIOR APPLICATION NUMBER: 08/801,248
;; PRIOR FILING DATE: 1997-02-19
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 6
;; LENGTH: 1315
;; TYPE: DNA
;; ORGANISM: Caenorhabditis elegans
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (7)...(846)
US-09-233-527-6

Query Match 99.8%; Score 1313; DB 4; Length 1315;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGATGACACGCTGACGCGGCAACACTGCTGACGAATTCGGCTATGCGGACGA 60
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1 TTGAGATGACACGCTGACGCGGCAACACTGCTGACGAATTCGGCTATGCGGACGA 60
DB 61 ACAGTGGCGACTGCGGAGATGAAGAGTTCGTGGGATTAAGAGCCACACACCGAT 120
|||||
61 ACAGTGGCGACTGCGGAGATGAAGAGTTCGTGGGATTAAGAGCCACACCGAT 120
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|||||
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|||||
181 AGAATGTCCTGCGAGAGTCAATTTGATGAAAAATCAATGATTTGGAGAACCCAGGCTT 240
DB 181 AGAATGTCCTGCGAGAGTCAATTTGATGAAAAATCAATGATTTGGAGAACCCAGGCTT 240
|||||
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QY 241 GATATGAGGAGATTTTGTGCTGACTATTTACGACGACCGAATCCGGAACGGAATGGA 300
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241 GATATGAGGAGATTTTGTGCTGACTATTTACGACGACCGAATCCGGAACGGAATGGA 300
DB 241 GATATGAGGAGATTTTGTGCTGACTATTTACGACGACCGAATCCGGAACGGAATGGA 300
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DB 301 TGGTTGGAGCACCGGAGATTCCGTGTGAGTGAAGTCAACCGAGACGAAATGATGCGAGTT 360
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301 TGGTTGGAGCACCGGAGATTCCGTGTGAGTGAAGTCAACCGAGACGAAATGATGCGAGTT 360
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361 ATGGGAACGATATTCGAGAAAGACGCGGAAATTTTGAGACCTTCTGTAGACGCTG 420
DB 361 ATGGGAACGATATTCGAGAAAGACGCGGAAATTTTGAGACCTTCTGTAGACGCTG 420
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361 ATGGGAACGATATTCGAGAAAGACGCGGAAATTTTGAGACCTTCTGTAGACGCTG 420
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421 CTCGACGTGCGGAGATTCATTTTCTACGTATCAGATGTTGGAGCGTTGGAAT 480
DB 421 CTCGACGTGCGGAGATTCATTTTCTACGTATCAGATGTTGGAGCGTTGGAAT 480
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541 GGTTCGTAGCTGCAAAATGATGATCCGTGAACTGCAAGGCAAGTCCGAAACCTC 600
DB 541 GGTTCGTAGCTGCAAAATGATGATCCGTGAACTGCAAGGCAAGTCCGAAACCTC 600
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541 GGTTCGTAGCTGCAAAATGATGATCCGTGAACTGCAAGGCAAGTCCGAAACCTC 600
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601 TTGCTTACACATCGCTGTTTCATCAAAACGCGGATCCGCAACACTGGAAGAACACAT 660
DB 601 TTGCTTACACATCGCTGTTTCATCAAAACGCGGATCCGCAACACTGGAAGAACACAT 660
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601 TTGCTTACACATCGCTGTTTCATCAAAACGCGGATCCGCAACACTGGAAGAACACAT 660
QY 661 CGGAGCTGGAGACTTCATGACATCGGAAACAAATGAAAGGAGACTAGGAAGAGCA 720
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661 CGGAGCTGGAGACTTCATGACATCGGAAACAAATGAAAGGAGACTAGGAAGAGCA 720

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Db 661 CGAGCTGGGACGACTTCATACACCTCGAAGCAAAATGAAAGAGGACTACGAGACGACA 720
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Db 781 GTAACAGCTGAGCATTGGAATCGTTGAGTCTGCTGTTGGCGGATGATGTTGACG 840
Qy 841 TTGAAGTACCTATTCATTTGTTGTAATTAATTAATTAATTAATTAATTAATTAATTA 900
Db 841 TTGAAGTACCTATTCATTTGTTGTAATTAATTAATTAATTAATTAATTAATTAATTA 900
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Db 901 ATTCATTTTGTCTACGATTTCTCTATCCTTTGAACTGGAAAGTGGAAAGCTAGG 960
Qy 961 CCACAAATTAACGCTCTCTGTGTGATTTAGATTTTACTGCAATTTTTCGATTCCT 1020
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Db 1141 CATTTCCAAAGTACCCCTGATATCAATTAATTAATTAATTAATTAATTAATTAATTA 1200
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Qy 1261 TTCAAAATGTTTCTCTCTACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1315
Db 1261 TTCAAAATGTTTCTCTCTACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1315

RESULT 10
US-09-234-186-1
; Sequence 1, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; EARLIER FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6559
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (1)...(6559)
; OTHER INFORMATION: n = A,T,C or G
US-09-234-186-1
Query Match 48.1%; Score 632.6; DB 4; Length 6559;
Best Local Similarity 99.8%; Pred. No. 2,9e-190;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 669 GAGACCTTCATGACACTCGGAAACAAATGAAAGAGACTACGACGACGAAAGCTGA 728
Db 3392 GAGACCTTCATGACACTCGGAAACAAATGAAAGAGACTACGACGACGAAAGCTGA 728
Qy 729 AAAAGTGGAGCGCCGAGACAGACAGACGCGTGGATGGCGCGGAGTAACG 788
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Qy 789 TGGAGCATTGGAATCGTTGAGTCTGCTGTTGGCGGATGATGTTGACGTTGAAGTA 848
Db 3512 TGGAGCATTGGAATCGTTGAGTCTGCTGTTGGCGGATGATGTTGACGTTGAAGTA 848
Qy 849 ACCTATTCATTTGTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 908
Db 3572 ACCTATTCATTTGTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 908
Qy 909 TTKGCTACATGATTTCTCTATCCTTTGAACTGGAAAGTGGAAAGCTAGGCGCAAT 968
Db 3632 TTKGCTACATGATTTCTCTATCCTTTGAACTGGAAAGTGGAAAGCTAGGCGCAAT 968
Qy 969 TACGGCTCTGTGTGATTTAGATTTTACTGCAATTTTTCGATTCCTTTTTCCTT 1028
Db 3692 TACGGCTCTGTGTGATTTAGATTTTACTGCAATTTTTCGATTCCTTTTTCCTT 1028
Qy 1029 GGGCAACCTTACTTCCGGTAATCAACTTTCCGTTCTGTACATTTTCGTAACAA 1088
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Qy 1089 CCTGAAACCTTACTTCTGCGGTGGCGTACGCTCCGCTTCTCTCCACATTTGCA 1148
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RESULT 11
US-09-233-527-1
; Sequence 1, Application US/09233527
; Patent No. 6465617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09/233,527
; EARLIER FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248

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1  APPLICANT: FALKNER, F. G.
2  TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
3  NUMBER OF SEQUENCES: 52
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Foley & Lardner
6  STREET: 1800 Diagonal Road, Suite 500
7  City: Alexandria
8  STATE: VA
9  COUNTRY: USA
10 ZIP: 22313-0299
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patentin Release #1.0, Version #1.25
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/232,463
19 FILING DATE:
20 CLASSIFICATION: 435
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US/07/935,313
23 FILING DATE:
24 APPLICATION NUMBER: EP 91 114 300.6
25 FILING DATE: 26-AUG-1991
26 ATTORNEY/AGENT INFORMATION:
27 NAME: BENT, Stephen A.
28 REGISTRATION NUMBER: 29,768
29 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (703)836-9300
32 TELEFAX: (703)683-4109
33 TELEX: 899149
34
35 INFORMATION FOR SEQ ID NO: 14:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 7218 base pairs
38 TYPE: nucleic acid
39 STRANDEDNESS: single
40 TOPOLOGY: linear
41 IMMEDIATE SOURCE:
42 CLONE: PT9pt-Fls
43
44 US-08-232-463-14

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

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(without alignments)
6280.048 Million cell updates/sec

Title: US-09-993-420A-2

Perfect score: 1315

Sequence: 1 tttagatgacacgctgcac.....cgttcaaaaaaaaaaaaaa 1315

Scoring table:

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Searched: 460893 seqs, 311809382 residues

Total number of hits satisfying chosen parameters: 921786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 6: /cgn2_6/ptodata/2/pubpna/PCUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	3.2	3160	9 US-10-098-841-273	Sequence 273, App
2	41	3.1	2000	9 US-09-938-842A-3764	Sequence 3764, App
3	39.8	3.0	425	10 US-09-834-975-451	Sequence 451, App
4	39.8	3.0	425	10 US-09-834-975-451	Sequence 451, App
5	39.6	3.0	458	10 US-09-770-444-474	Sequence 474, App
6	39.4	3.0	1680	9 US-09-986-480-20	Sequence 20, Appl
7	38.6	2.9	418	10 US-09-960-352-4845	Sequence 4845, App
8	38	2.9	608	10 US-09-770-145-884	Sequence 884, App
9	37	2.8	312	10 US-09-960-352-8414	Sequence 8414, App
10	37	2.8	410	10 US-09-960-352-4438	Sequence 4438, App
11	37	2.8	630	10 US-09-925-300-548	Sequence 548, App
12	37	2.8	180216	10 US-09-835-232-6	Sequence 6, Appl
13	36.8	2.8	387	10 US-09-867-701-10218	Sequence 10218, A
14	36.8	2.8	459	9 US-10-015-219-777	Sequence 777, App
15	36.8	2.8	459	10 US-09-777-564-777	Sequence 777, App
16	36.8	2.8	517	9 US-10-015-219-1649	Sequence 1649, App
17	36.8	2.8	517	10 US-09-777-564-1649	Sequence 1649, App
18	36.8	2.8	566	9 US-09-796-692-4903	Sequence 4903, App
19	36.8	2.8	727	9 US-10-202-193-281	Sequence 281, App

20	36.8	2.8	751	9 US-10-202-193-280	Sequence 280, App
21	36.8	2.8	773	9 US-10-202-193-176	Sequence 176, App
22	36.8	2.8	2361	10 US-09-925-299-59	Sequence 59, Appl
23	36.6	2.8	396	9 US-09-970-966-10	Sequence 10, Appl
24	36.6	2.8	396	10 US-09-825-294-10	Sequence 10, Appl
25	36.4	2.8	312	10 US-09-960-352-8414	Sequence 8414, App
26	36.4	2.8	742	9 US-09-950-9338-35	Sequence 35, Appl
27	36	2.7	1531	10 US-09-925-300-577	Sequence 577, App
28	35.8	2.7	221	10 US-09-864-761-18315	Sequence 18315, A
29	35.8	2.7	487	10 US-09-864-761-1556	Sequence 1556, App
30	35.6	2.7	253	10 US-09-778-320-124	Sequence 124, App
31	35.6	2.7	253	10 US-09-910-689-124	Sequence 124, App
32	35.6	2.7	253	12 US-10-010-742-124	Sequence 124, App
33	35.6	2.7	373	10 US-09-960-352-16676	Sequence 14676, A
34	35.6	2.7	202001	10 US-09-734-674-3	Sequence 3, Appl
35	35.4	2.7	1307	10 US-09-250-611-3	Sequence 3, Appl
36	35.4	2.7	2000	9 US-09-938-842A-2926	Sequence 2926, App
37	35.4	2.7	4019	10 US-09-764-847-1431	Sequence 1431, App
38	35.2	2.7	160	10 US-09-783-590-3161	Sequence 3161, App
39	35.2	2.7	1120	10 US-09-070-921A-721	Sequence 721, App
40	35	2.7	308	10 US-09-960-352-7670	Sequence 7670, App
41	35	2.7	1053	10 US-09-925-302-53	Sequence 53, Appl
42	34.8	2.6	392	10 US-09-960-352-2634	Sequence 2634, App
43	34.8	2.6	416	10 US-09-960-352-4584	Sequence 4584, App
44	34.8	2.6	418	10 US-09-960-352-4845	Sequence 4845, App
45	34.8	2.6	424	10 US-09-960-352-11218	Sequence 11218, A

ALIGNMENTS

RESULT 1
US-10-098-841-273
; Sequence 273, Application US/10098841
; Publication No. US20020197679A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungling
; APPLICANT: Wang, Qian-Rui
; APPLICANT: Zhao, Jing A.
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020197679A1 Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/10/098,841
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: pt_files Version 1.0
; SEQ ID NO 273
; LENGTH: 3160
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (169)..(1092)
; US-10-098-841-273


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? APPLICANT: Price, Jennifer L.
? APPLICANT: Raines, Tracy M.
? APPLICANT: Yu, Yang
? APPLICANT: Rameaka, Joshua G.
? APPLICANT: Page, Amy
? APPLICANT: Matthew, Abraham V.
? APPLICANT: Ledford, Brooke L.
? APPLICANT: Woessner, Jeffrey P.
? APPLICANT: Haas, William David
? APPLICANT: Garcia, Carlos A.
? APPLICANT: Kicker, Maja
? APPLICANT: Slader, Ted
? APPLICANT: Davis, Keith R.
? APPLICANT: Allen, Keith
? APPLICANT: Hoffman, Neil
? APPLICANT: Hurban, Patrick
? TITLE OF INVENTION: Expressed Sequences of Arabidopsis
? TITLE OF INVENTION: Thaliana
? FILE REFERENCE: 2027 (PARA-016PRV)
? CURRENT APPLICATION NUMBER: US/09/770,444
? PRIOR FILING DATE: 2001-01-26
? PRIOR FILING DATE: 2000-01-27
? NUMBER OF SEQ. ID NOS: 999
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ. ID NO 474
? LENGTH: 458
? TYPE: DNA
? ORGANISM: Arabidopsis thaliana
? US-09-770-444-474

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						Indels 74; Gaps 0;
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QY	1218	CCCCCAATTCCTGTACGGCGTACGGCACTTGTATTTATTTTTTCCAATTTGTTTTCT	1277			
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Db	82	TTTTGTATAAAAAAAAAAAAAAAAAAAAAA	45			

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RESULT 6
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/ Sequence 20, Application US/09986480
/ Publication No. US2003002799A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: 143 Human Secreted Proteins
/ FILE REFERENCE: P5500P1
/ CURRENT APPLICATION NUMBER: US/09/986,480
/ CURRENT FILING DATE: 2001-11-08
/ PRIOR APPLICATION NUMBER: PCT/US00/12788
/ PRIOR FILING DATE: 2000-05-11
/ PRIOR APPLICATION NUMBER: US 60/134,068
/ PRIOR FILING DATE: 1999-05-13
/ NUMBER OF SEQ ID NOS: 456
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 20
/ LENGTH: 1680
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (1673)
/ OTHER INFORMATION: n equals a,l,g, or c
/ NAME/KEY: SITE

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Best Local Similarity	65.28;	Pred. No. 0.99;		
Matches 58;	Conservative 0;	Mismatches 31;	Indels 0;	Gaps 0;

QY	1227	TCTGTACCCGACGAGCATTTGTATTTTTCATTTTTCATATTTGTTTCTCTACAAACA	1286
	1562	TCCCCGACGTGACGTGACGTTTTTTAAATTAATAAATGTTTATTATTAACAATG	1621
QY	1287	CAAAAAAAGCGTTCAAAAAATAAAAAA	1315
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Db			

RESULT 7
 US-09-960-352-4845
 ; Sequence 4845, Application US/09960352
 ; Patent No. US20020137139A1
 GENERAL INFORMATION

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1  APPLICANT: Warren, Wesley C.
2  APPLICANT: Tao, Nengping
3  APPLICANT: Byalt, John C.
4  APPLICANT: Mathialagan, Nagappan
5  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION
6  TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
7  FILE REFERENCE: 16511.006/37-21(10298)C
8  CURRENT APPLICATION NUMBER: US/09/960,352
9  CURRENT FILING DATE: 2001-09-24
10 NUMBER OF SEQ ID NOS: 15112
11 SEQ ID NO 4845
12
13 LENGTH: 418
14
15 TYPE: DNA
16
17 ORGANISM: Bos taurus
18
19 OTHER INFORMATION: Clone ID: 21-LIB3056-035-Q1-K1-P9
20
21 US-09-960-352-4845

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Query Match	2.9%;	Score 38.6;	DB 10;	Length 418;
Best Local Similarity	72.5%;	Pred. No. 0.81;	Mismatches 19;	Indels 0;
Matches 50;	Conservative	0;	Gaps 0;	
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1306	AAAAAAAAA	1314		
202				
139	TAATAAAAAA	147		

RESULT 8
 US-09-770-149-894/c
 Sequence 894, Application US/09770149
 Patent No. US20020059653A1
 GENERAL INFORMATION:
 APPLICANT: Gorlach, Jorn
 APPLICANT: An, Yong-Qiang
 APPLICANT: Hamilton, Carol M.
 APPLICANT: Price, Jennifer L.
 APPLICANT: Raines, Tracy M.
 APPLICANT: Yu, Yang
 APPLICANT: Rameaka, Joshua G.
 APPLICANT: Page, Amy
 APPLICANT: Matthew, Abraham V.
 APPLICANT: Ledford, Brooke L.
 APPLICANT: Moessner, Jeffrey P.
 APPLICANT: Haas, William David
 APPLICANT: Garcia, Carlos A.

Query Match	2.88;	Score 37;	DB 10;	Length 312;
Best Local Similarity	71.08;	Pred. NO. 1.9;	20;	Indels 0;
Matches 49;	Conservative	0;	Mismatches	Gaps 0;
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DB 80	AAAAAAAAAA 72			

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RESULT 11
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; Sequence 548, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-548

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			Indels	0;
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Db 530	GTACCTCACCCTTAGTTGATTTCCCTATTATAAGTATATTTTCTATAGAAAAAAA	589		
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Query Match	2.8%	Score 36.8	DB 10	Length 459
Best Local Similarity	61.5%	Pred. No. 2.6		
Matches 59; Conservative	0;	Mismatches 37;	Indels 0;	Gaps 0;

QY	1220	CCCAATTCCTGACCGCGACGCACTGATATATTTTTCGAATTTCTTCTCTCT	1279
Db	185	CCAGCATTTCTGCGAATTCATCGAATTTTCTTTCTTTGTAATTAATAATCTCTCTCT	126

Thu Mar 6 08:14:04 2003

us-09-993-420a-2.rnpb

Page 6

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| | | | | | | | | | | | | | |
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Job time : 188.582 secs

GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 20:03:45 ; Search time 2495.41 Seconds

(without alignments)
13249.270 Million cell updates/sec

Title: US-09-993-420A-2

Perfect score: 1315

Sequence: 1 ttgagatgacacgctgcac.....cgttcaaaaaaaaaaaaaa 1315

Scoring table:

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Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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Printed. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1314.6	100.0	1315	US-07-927-681-2	Sequence 2, Appl
2	1314.6	100.0	1315	US-08-288-295-2	Sequence 2, Appl
3	1314.6	100.0	1315	US-08-801-248-2	Sequence 2, Appl
4	1314.6	100.0	1315	US-09-993-420A-2	Sequence 2, Appl
5	1313	99.8	1315	US-08-288-295-4	Sequence 4, Appl
6	1313	99.8	1315	US-08-288-295-5	Sequence 5, Appl
7	1313	99.8	1315	US-08-288-295-6	Sequence 6, Appl
8	1313	99.8	1315	US-08-801-248-4	Sequence 4, Appl
9	1313	99.8	1315	US-08-801-248-5	Sequence 5, Appl
10	1313	99.8	1315	US-08-801-248-6	Sequence 6, Appl
11	1313	99.8	1315	US-09-993-420A-4	Sequence 4, Appl
12	1313	99.8	1315	US-09-993-420A-5	Sequence 5, Appl
13	1313	99.8	1315	US-09-993-420A-6	Sequence 6, Appl
14	632.6	48.1	6559	US-07-927-681-1	Sequence 1, Appl
15	632.6	48.1	6559	US-08-288-295-1	Sequence 1, Appl
16	632.6	48.1	6559	US-08-801-248-1	Sequence 1, Appl
17	632.6	48.1	6559	US-09-993-420A-1	Sequence 1, Appl
18	81.8	6.2	7218	US-08-466-194-14	Sequence 14, Appl
19	57.2	4.3	470	US-09-865-419A-35584	Sequence 35584, A
20	57.2	4.3	470	US-60-208-063-18643	Sequence 18643, A
21	55.6	4.2	7218	US-08-466-194-14	Sequence 14, Appl

Db 961 CCACAAATTAAGGCTCTCTGTGCAATTTAGCATTTTTCGCAATTTTTCGATTCCT 1020
 Qy 1021 TTTTGTGGCCAAACCCCTACTTCCGGTATATCACTTTTCCGTTCTGTACATTC 1080
 Db 1021 TTTTGTGGCCAAACCCCTACTTCCGGTATATCACTTTTCCGTTCTGTACATTC 1080
 Qy 1081 GTCAAAAACCCCTGAACCTTAATTTCTGCGCGTACGCTCCGCTTCCTTCCA 1140
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 Qy 1141 CATTTCAAGTACCCCTGTATGTCATTAATTCATCTTCACTTAACTGTCTTTTCT 1200
 Db 1141 CATTTCAAGTACCCCTGTATGTCATTAATTCATCTTCACTTAACTGTCTTTTCT 1200
 Qy 1201 GTGGCCCTTTCACACTCCGCCAAATTCCTGTAGCGGTACGAGCTTGTATTTT 1260
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 Qy 1261 TTCAAAATTTTCTCTCTACACAACAAAAAAGCGTTCAAAAAA 1315
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RESULT 2

US-08-288-295-2

Sequence 2, Application US/08288295

GENERAL INFORMATION:

APPLICANT: Horvitz, H. Robert

APPLICANT: Hengartner, Michael

TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A

TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & RICHARDSON

STREET: 225 Franklin Street, Suite 3100

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A. (F) ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/288,295

FILING DATE: 10-AUG-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,681

FILING DATE: 10-AUG-1992

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 01997/201003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1315 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

FEATURE:

NAME/KEY: CDS

LOCATION: 7..846

OTHER INFORMATION: /product= "Ced-9"

Query Match 100.0%; Score 1314.6; DB 6; Length 1315;
 Best Local Similarity 100.0%; Pred. No. 1.5e-288;
 Matches 1315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTGAGATGACACGCTGACGCGGAGCAACCTGCTGACGAATCCGGATATGGGAGAGA 60
 Db 1 TTTGAGATGACACGCTGACGCGGAGCAACCTGCTGACGAATCCGGATATGGGAGAGA 60
 Qy 61 ACAGATGCGAGTGGCGAGATGAAGAGTTTCTGGGGATTAAGGACAGAGCCACGAT 120
 Db 61 ACAGATGCGAGTGGCGAGATGAAGAGTTTCTGGGGATTAAGGACAGAGCCACGAT 120
 Qy 121 TTTGGAATCAATAGTAGTCTCAGAGCTTGGCATACCGAGATGAGGAGCTTTCAGCGGA 180
 Db 121 TTTGGAATCAATAGTAGTCTCAGAGCTTGGCATACCGAGATGAGGAGCTTTCAGCGGA 180
 Qy 181 AGAATGTCATCGAGAGTCAATTTATGAAATAATCAATGATTTGGAAGCCAAAGCTT 240
 Db 181 AGAATGTCATCGAGAGTCAATTTATGAAATAATCAATGATTTGGAAGCCAAAGCTT 240
 Qy 241 GATATCGAGGATTTGTGTCATTTTCAAGCAGCAGCAATCCGGCAAAACGGAATGGA 300
 Db 241 GATATCGAGGATTTGTGTCATTTTCAAGCAGCAGCAATCCGGCAAAACGGAATGGA 300
 Qy 301 TGGTTTGAGACACCGGATTTCCCGTGTGAGTGCACCGGACAGCAAGATGATCGAGTT 360
 Db 301 TGGTTTGAGACACCGGATTTCCCGTGTGAGTGCACCGGACAGCAAGATGATCGAGTT 360
 Qy 361 ATGGGAAGATATTCGAGAAAGACAGCGGCAAAATTTTGAAGCTTCTGTAGCAGCTG 420
 Db 361 ATGGGAAGATATTCGAGAAAGACAGCGGCAAAATTTTGAAGCTTCTGTAGCAGCTG 420
 Qy 421 CTCGAGTGCAGCAATCTATTTTCACTGATGAGATGTTGTTGAGCGGTTGGAAT 480
 Db 421 CTCGAGTGCAGCAATCTATTTTCACTGATGAGATGTTGTTGAGCGGTTGGAAT 480
 Qy 481 GCACAGACAGATCAATGCTCAATGCTTTATGAGCTTTGATAGTCTAATCTGTTGCGC 540
 Db 481 GCACAGACAGATCAATGCTCAATGCTTTATGAGCTTTGATAGTCTAATCTGTTGCGC 540
 Qy 541 GGTTCGTAGCTGCAAAATGATGAGATCCGTGGAATCGTAGGAGCAAGTGCAGAACTTC 600
 Db 541 GGTTCGTAGCTGCAAAATGATGAGATCCGTGGAATCGTAGGAGCAAGTGCAGAACTTC 600
 Qy 601 TTGCTTTACATCGCTGTTTCAATCAAAACGCGGATCCGCAACTGGAAGAACCAAT 660
 Db 601 TTGCTTTACATCGCTGTTTCAATCAAAACGCGGATCCGCAACTGGAAGAACCAAT 660
 Qy 661 CGGAGCTGGAGACATTCATGACACTCGGAAACCAATGAAGAGACTACGAAACAGAGA 720
 Db 661 CGGAGCTGGAGACATTCATGACACTCGGAAACCAATGAAGAGACTACGAAACAGAGA 720
 Qy 721 GAAGCTGAAAAAGTGGAGCCGGAAGACAGAGAGGTTGATGATTTGGCGTGA 780
 Db 721 GAAGCTGAAAAAGTGGAGCCGGAAGACAGAGAGGTTGATGATTTGGCGTGA 780
 Qy 781 GTAAAGCTGGAGACATTTGAATGCTTTGAGAGTGTGTGTGGGCGGATGATTTTACG 840
 Db 781 GTAAAGCTGGAGACATTTGAATGCTTTGAGAGTGTGTGTGGGCGGATGATTTTACG 840
 Qy 841 TTGAAGTAAAGTAATTTGTAATTAATTAATTTTGAACAGTCTTACATTTGA 900
 Db 841 TTGAAGTAAAGTAAATTTGTAATTAATTAATTTTGAACAGTCTTACATTTGA 900
 Qy 901 ATCTCATTTTTCCTCATCTATCTCATCTTTGAACGGAAGGAGGAAAGCTAGG 960
 Db 901 ATCTCATTTTTCCTCATCTATCTCATCTTTGAACGGAAGGAGGAAAGCTAGG 960
 Qy 961 CCACAAATTAAGGCTCTGTGTCATTTTACGATTTTACGATTTTTCGATTCCT 1020
 Db 961 CCACAAATTAAGGCTCTGTGTCATTTTACGATTTTACGATTTTTCGATTCCT 1020
 Qy 1021 TTTTGTGGCCAAACCCCTACTTCCGGTATATCACTTTTCCGTTCTGTACATTC 1080

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Db 1021 TTTTGGGCAACCTACTCTCGGTAAATCAACTTTCGCTGTCTGTACATTTCC 1080
Oy 1081 GTCAAAAACCCCTGAACCTTAATCTTTCGCGCTGAGCTTCCGCTTCCTTCCA 1140
Db 1081 GTCAAAAACCCCTGAACCTTAATCTTTCGCGCTGAGCTTCCGCTTCCTTCCA 1140
Oy 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATCACTTCACTTCACTGCTCTTTCGT 1200
Db 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATCACTTCACTTCACTGCTCTTTCGT 1200
Oy 1201 GAGGCTCTTCCACTCCCTCCCAATTCCTGTAGCGGTACGCGACTTGTATTTT 1260
Db 1201 GAGGCTCTTCCACTCCCTCCCAATTCCTGTAGCGGTACGCGACTTGTATTTT 1260
Oy 1261 TTCAATTTGTTTCTCTCTACCAACAACAAAAACGGTTCAAAAA 1315
Db 1261 TTCAATTTGTTTCTCTCTACCAACAACAAAAACGGTTCAAAAA 1315

RESULT 3
US-08-801-248-2
Sequence 2, Application US/08801248
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Hengartner, Michael
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
TITLE OF INVENTION: CELL DEATH AND USES THEREFOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FISH & RICHARDSON
STREET: 225 Franklin Street, Suite 3100
City: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,248
FILING DATE: 19-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/288,295
FILING DATE: 10-AUG-1994
APPLICATION NUMBER: US 07/927,681
FILING DATE: 10-AUG-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 01997/201003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1315 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 7..846
OTHER INFORMATION: /product= "Ced-9"
US-08-801-248-2

```

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Query Match      100.0%; Score 1314.6; DB 12; Length 1315;
Best Local Similarity 100.0%; Pred. No. 1.5e-288;
Matches 1315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTTGAGATGACAGCTGACAGCGGAGCAACTGCTGACGAATTCGGCGTATGCGGACGA 60
Db 1 TTTGAGATGACAGCTGACAGCGGAGCAACTGCTGACGAATTCGGCGTATGCGGACGA 60
Oy 61 ACGATGCGGAGTGGCGGATGGAAGAGAGTTCGCGATTAAGAGCAGAGCCACCAT 120
Db 61 ACGATGCGGAGTGGCGGATGGAAGAGAGTTCGCGATTAAGAGCAGAGCCACCAT 120
Oy 121 TTTGGAATCAATAGTGAATGCTCAGAGCTTGCATCAACCGATGAGGAGGCTTCGACGCA 180
Db 121 TTTGGAATCAATAGTGAATGCTCAGAGCTTGCATCAACCGATGAGGAGGCTTCGACGCA 180
Oy 181 AGAATGTCATGAGAGTCAATTTGATGAAAAATCAATATTTGGGAAGGCCAAGGCTT 240
Db 181 AGAATGTCATGAGAGTCAATTTGATGAAAAATCAATATTTGGGAAGGCCAAGGCTT 240
Oy 241 GATATCGAGGATTTGGTGTGACTATTTACGACCGCAATCCGGCAAAACGGAATGGA 300
Db 241 GATATCGAGGATTTGGTGTGACTATTTACGACCGCAATCCGGCAAAACGGAATGGA 300
Oy 301 TGGTTTGAGGACCGGAGATTGCGGTGAGTGCACACCGAGCAAAATGATCGGAGTT 360
Db 301 TGGTTTGAGGACCGGAGATTGCGGTGAGTGCACACCGAGCAAAATGATCGGAGTT 360
Oy 361 ATGGAACGATATTCGAAGAAGCAGCGGAAATTTTGAGACCTTCTGTGACACCTG 420
Db 361 ATGGAACGATATTCGAAGAAGCAGCGGAAATTTTGAGACCTTCTGTGACACCTG 420
Oy 421 CTCGAGTGCACAGATCTATTTCTACTGTATGAGATGATGTTGCGACGTTGGAAAT 480
Db 421 CTCGAGTGCACAGATCTATTTCTACTGTATGAGATGATGTTGCGACGTTGGAAAT 480
Oy 481 GCACAGACAGATCAATTCATCTCTATGAGCTTATGATGCTATATCTCGTTGCGC 540
Db 481 GCACAGACAGATCAATTCATCTCTATGAGCTTATGATGCTATATCTCGTTGCGC 540
Oy 541 GGTTCGTAGTGTCAAAAATGATGGAATCCGTGAACTGACAGGACCAAGTGCAGAACTC 600
Db 541 GGTTCGTAGTGTCAAAAATGATGGAATCCGTGAACTGACAGGACCAAGTGCAGAACTC 600
Oy 601 TTGCTTACATCGCTGTTCATCAAAAACGGGATCCGCAACACTGGAAGACACAT 660
Db 601 TTGCTTACATCGCTGTTCATCAAAAACGGGATCCGCAACACTGGAAGACACAT 660
Oy 661 CGAGCTGGAGAGCTTCAATGACACTGGAACCAATGAAGAGACTACGAAGACGA 720
Db 661 CGAGCTGGAGAGCTTCAATGACACTGGAACCAATGAAGAGACTACGAAGACGA 720
Oy 721 GAAGCTGAAAAAGTGGAGCGCGGAAGCAACAGACGCTGCTCATGTTGGCGCTGGA 780
Db 721 GAAGCTGAAAAAGTGGAGCGCGGAAGCAACAGACGCTGCTCATGTTGGCGCTGGA 780
Oy 781 GTAAACGCTGAGCCATGGAATGCTTGGAGTGTGCTGTGGGCGAGTATGTTCAAC 840
Db 781 GTAAACGCTGAGCCATGGAATGCTTGGAGTGTGCTGTGGGCGAGTATGTTCAAC 840
Oy 841 TTGAAGTAACGTATTCATTTGTAAATTAATTAATTAATTAATTAATTAATTAATTA 900
Db 841 TTGAAGTAACGTATTCATTTGTAAATTAATTAATTAATTAATTAATTAATTAATTA 900
Oy 901 ATCTCATTTTGGCTCACTGATTTCTCTCATCTTGAAGTGAAGTGAAGTGAAGTGA 960
Db 901 ATCTCATTTTGGCTCACTGATTTCTCTCATCTTGAAGTGAAGTGAAGTGAAGTGA 960
Oy 961 CCACAAATTAAGGCTCTCTGTGATGATTTAGATTTTACTGCAATTTTTCGATGCT 1020
Db 961 CCACAAATTAAGGCTCTCTGTGATGATTTAGATTTTACTGCAATTTTTCGATGCT 1020
Oy 1021 TTTTGGCAACCTACTTCCGCTAATATCAACTTTCGGTGTCTGTACATTTTC 1080

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Db 1021 TTTTGGGCAACCTACTCCGGTATATCACTTTTCGTTCTGTACATTTTC 1080
Qy 1081 GTCAAAAACCCGSAACCCCTACTTTCTGCGCGTGGCTAGCCCTCCGCTCTCTCCA 1140
Db 1081 GTCAAAAACCCCTGAAACCCCTACTTTCTGCGCGTGGCTAGCCCTCCGCTCTCTCCA 1140
Qy 1141 CATTTCAAAAGTACCCCTGTATCTCAATATTCATCTTCACTTTAATGTCCTTTTCGT 1200
Db 1141 CATTTCAAAAGTACCCCTGTATCTCAATATTCATCTTCACTTTAATGTCCTTTTCGT 1200
Qy 1201 GTGGCTCTTCCACCTCCGCAAAATTCGTACGCGGTACGCGACTTTGATTTATTTT 1260
Db 1201 GTGGCTCTTCCACCTCCGCAAAATTCGTACGCGGTACGCGACTTTGATTTATTTT 1260
Qy 1261 TTCAAAATGTTTCTCTCTACACACAAACCAAAAGGTTCAAAAACCAAA 1315
Db 1261 TTCAAAATGTTTCTCTCTACACACAAACCAAAAGGTTCAAAAACCAAA 1315

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RESULT 4

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US-09-993-420a-2
: Sequence 2, Application US/09993420A
: GENERAL INFORMATION:
: APPLICANT: Horvitz, H. Robert
: APPLICANT: Hengartner, Michael
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
: TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: 01997/201006
: CURRENT APPLICATION NUMBER: US/09/993,420A
: PRIOR FILING DATE: 5001-11-09
: PRIOR APPLICATION NUMBER: 09/234,186
: PRIOR FILING DATE: 1999-01-20
: PRIOR APPLICATION NUMBER: 07/898,933
: PRIOR FILING DATE: 1992-06-12
: PRIOR APPLICATION NUMBER: 07/927,681
: PRIOR FILING DATE: 1992-08-10
: PRIOR APPLICATION NUMBER: 08/288,295
: PRIOR FILING DATE: 1994-08-10
: PRIOR APPLICATION NUMBER: 08/801,248
: PRIOR FILING DATE: 1997-02-19
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 1315
: TYPE: DNA
: ORGANISM: Caenorhabditis elegans
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (7)...(846)
: US-09-993-420a-2

```

```

Query Match      100.0%; Score 1314.6; DB 37; Length 1315;
Best Local Similarity 100.0%; Pred. No. 1.5e-288;
Matches 1315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 TTTGAGATGACACCTCTGACGCGGACACACACGCTGACGATCCGCGATGCGGAGCA 60
Db 1 TTTGAGATGACACCTCTGACGCGGACACACACGCTGACGATCCGCGATGCGGAGCA 60
Qy 61 ACGATGGCGACCTGGCGGATGAAAGAGTTTCTGGGATATAAAGGCAACAAGCCACCGAT 120
Db 61 ACGATGGCGACCTGGCGGATGAAAGAGTTTCTGGGATATAAAGGCAACAAGCCACCGAT 120
Qy 121 TTTGGAATCATATAGTATGCTCAGACTTGGCCATCCGAGATAGGAGAGCTTGCAGCGCA 180
Db 121 TTTGGAATCATATAGTATGCTCAGACTTGGCCATCCGAGATAGGAGAGCTTGCAGCGCA 180
Qy 181 AGAATGTCATCGGAGAGTCAATTTGATGAAAAATCAATGATTTGGAGAGCAAGGCTT 240
Db 181 AGAATGTCATCGGAGAGTCAATTTGATGAAAAATCAATGATTTGGAGAGCAAGGCTT 240

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Qy 241 GATATGAGGATTTGGTGGACTATTTCACGACCGAATCCGGCAAAACGSAATGAA 300
Db 241 GATATGAGGATTTGGTGGACTATTTCACGACCGAATCCGGCAAAACGSAATGAA 300
Qy 301 TGGTTTGAGGACCGGGAATTCGCGTGGAGTGCACACCGGAGCAGCAAAATGATGGAGTT 360
Db 301 TGGTTTGAGGACCGGGAATTCGCGTGGAGTGCACACCGGAGCAGCAAAATGATGGAGTT 360
Qy 361 ATGGAGAGATATTCGAGAAAGACACGCGGAAATTTTGAGACCTTGTGAGCAGCTG 420
Db 361 ATGGAGAGATATTCGAGAAAGACACGCGGAAATTTTGAGACCTTGTGAGCAGCTG 420
Qy 421 CTGCGAGTGGCCAGAAATCTTCACTGTATCAGATGATGGTTGCGAGGCTTGGAAAT 480
Db 421 CTGCGAGTGGCCAGAAATCTTCACTGTATCAGATGATGGTTGCGAGGCTTGGAAAT 480
Qy 481 GCACAGACATATCAATGTCATATGTCCTTATGACGTTTGAATGATGATCTATCTCGTGGC 540
Db 481 GCACAGACATATCAATGTCATATGTCCTTATGACGTTTGAATGATGATCTATCTCGTGGC 540
Qy 541 GGTTCGTAGCTCAAAAATGATGAAATCGTGAATCGTGAACGAGGACAGTGGAAACCTC 600
Db 541 GGTTCGTAGCTCAAAAATGATGAAATCGTGAATCGTGAACGAGGACAGTGGAAACCTC 600
Qy 601 TTGCTTTACATCGCTGTTTCATCAAAACGCGATCCGCAACACTGSAAGSAACACAT 660
Db 601 TTGCTTTACATCGCTGTTTCATCAAAACGCGATCCGCAACACTGSAAGSAACACAT 660
Qy 661 CGAGCTGGGAGACCTTCATGACACACGSAACCAATGAAAGAGAGACTACAGACAGCA 720
Db 661 CGAGCTGGGAGACCTTCATGACACACGSAACCAATGAAAGAGAGACTACAGACAGCA 720
Qy 721 GAAGCTGAAAAAGTGGGAGCCGGAAGCAAGAACAGACGCTGTGATGATGGGCGTGA 780
Db 721 GAAGCTGAAAAAGTGGGAGCCGGAAGCAAGAACAGACGCTGTGATGATGGGCGTGA 780
Qy 781 GTAACAGCTGAGGACATTTGGAATTCGTTGAGTCTGTGTGGCGGAGATGGTTCAGC 840
Db 781 GTAACAGCTGAGGACATTTGGAATTCGTTGAGTCTGTGTGGCGGAGATGGTTCAGC 840
Qy 841 TTGAAGTAACGATTTCAATTTGTGAAATTAATTAATTAATTAATTAATTAATTAATTA 900
Db 841 TTGAAGTAACGATTTCAATTTGTGAAATTAATTAATTAATTAATTAATTAATTAATTA 900
Qy 901 ATCTGATTTTGTCTACGATTTCTCTATCTCTATCTCTATCTCTATCTCTATCTCTATCT 960
Db 901 ATCTGATTTTGTCTACGATTTCTCTATCTCTATCTCTATCTCTATCTCTATCTCTATCT 960
Qy 961 CCACAAATTAAGGCTCTCTGTGTGATTTAGCAATTTTACGCAATTTTTCGATTTGCTT 1020
Db 961 CCACAAATTAAGGCTCTCTGTGTGATTTAGCAATTTTACGCAATTTTTCGATTTGCTT 1020
Qy 1021 TTTTGGGCAAAACCTACTCCGGTATATCACTTTTCGCTGTGATATTTTC 1080
Db 1021 TTTTGGGCAAAACCTACTCCGGTATATCACTTTTCGCTGTGATATTTTC 1080
Qy 1081 GTCAAAAACCCGTAACCCCTATCTTCTGCGCGTGGCTAGCCCTCCGCTCTCTCCA 1140
Db 1081 GTCAAAAACCCGTAACCCCTATCTTCTGCGCGTGGCTAGCCCTCCGCTCTCTCCA 1140
Qy 1141 CATTTCAAAAGTACCCCTGTATCTCAATATTCATCTTCACTTTAATGTCCTTTTCGT 1200
Db 1141 CATTTCAAAAGTACCCCTGTATCTCAATATTCATCTTCACTTTAATGTCCTTTTCGT 1200
Qy 1201 GTGGCTCTTCCACCTCCGCAAAATTCGTACGCGGTACGCGACTTTGATTTATTTT 1260
Db 1201 GTGGCTCTTCCACCTCCGCAAAATTCGTACGCGGTACGCGACTTTGATTTATTTT 1260
Qy 1261 TTCAAAATGTTTCTCTCTACACAAACCAAAAGGTTCAAAAACCAAA 1315
Db 1261 TTCAAAATGTTTCTCTCTACACAAACCAAAAGGTTCAAAAACCAAA 1315

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RESULT 5
US-08-288-295-4

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: Sequence 4, Application US/08288295
: GENERAL INFORMATION:
: APPLICANT: Horvitz, H. Robert
: APPLICANT: Hengartner, Michael
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
: TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
: TITLE OF INVENTION: CELL DEATH AND USES THEREFOR
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FISH & RICHARDSON
: STREET: 225 Franklin Street, Suite 3100
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A. (F) ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/288,295
: FILING DATE: 10-AUG-1994
: CLASSIFICATION: 514
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/927,681
: FILING DATE: 10-AUG-1992
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul F.
: REGISTRATION NUMBER: 30,162
: REFERENCE/DOCKET NUMBER: 01997/201003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-5070
: TELEFAX: (617) 542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1315 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 7..846
: OTHER INFORMATION: /product= "Ced-9"
: US-08-288-295-4

```

Query Match 99.8% Score 1313; DB 6; Length 1315;
Best Local Similarity 99.9%; Pred. No. 3.5e-288;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 TTTGAGATGACACGCTGACGCGGACAACTGCTGACGAATCCGGGCTATCGCGAGCA 60
    |||||||
DB 1 TTTGAGATGACACGCTGACGCGGACAACTGCTGACGAATCCGGGCTATCGCGAGCA 60
OY 61 ACGATGCGGACGCGGAGATGAAAGAGTTCTGGGATATAAAGGACAGACCCACCGAT 120
    |||||||
DB 61 ACGATGCGGACGCGGAGATGAAAGAGTTCTGGGATATAAAGGACAGACCCACCGAT 120
OY 121 TTTGGAATCAATAGTATGCTCAGACTTGCATCACCAGTAGGACGCTTGCAGCGCA 180
    |||||||
DB 121 TTTGGAATCAATAGTATGCTCAGACTTGCATCACCAGTAGGACGCTTGCAGCGCA 180
OY 181 ACGATGCTCCATGAGAGTCAATTTGATGAAAAATCAATGATTTGGAGAGCAAGGCTT 240
    |||||||
DB 181 ACGATGCTCCATGAGAGTCAATTTGATGAAAAATCAATGATTTGGAGAGCAAGGCTT 240
OY 241 GATATGAGGAGATTTGGTGCATTTTACGACCGAATCCGGCAAAAGGAAATGGAA 300
    |||||||
DB 241 GATATGAGGAGATTTGGTGCATTTTACGACCGAATCCGGCAAAAGGAAATGGAA 300

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OY 301 TGGTTTGAGACACCGGATTTGCCGTGTGGAGTGCACACCGACAGAAATGATGCGAGT 360
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DB 301 TGGTTTGAGACACCGGATTTGCCGTGTGGAGTGCACACCGACAGAAATGATGCGAGT 360
OY 361 ATGGAGACGATATTCAGAGAAGACACGCGGAAATTTTGGACCTTCTGTAGACAGCTG 420
    |||||||
DB 361 ATGGAGACGATATTCAGAGAAGACACGCGGAAATTTTGGACCTTCTGTAGACAGCTG 420
OY 421 CTCGACGTGCCCCAGATTCATTTTACGTGTATCAGATGTGTGTGAGCGGTTGGAAT 480
    |||||||
DB 421 CTCGACGTGCCCCAGATTCATTTTACGTGTATCAGATGTGTGTGAGCGGTTGGAAT 480
OY 481 GCACAGACGATCAATGCTCCATGCTTATGACGCTTTGATGATGCTAATCTCTGTCGCG 540
    |||||||
DB 481 GCACAGACGATCAATGCTCCATGCTTATGACGCTTTGATGATGCTAATCTCTGTCGCG 540
OY 541 GGTTCGTAGCTGCAAAATGATGGAATCCGTGACACTGAGGAGCAAGTGCNAACCTC 600
    |||||||
DB 541 GGTTCGTAGCTGCAAAATGATGGAATCCGTGACACTGAGGAGCAAGTGCNAACCTC 600
OY 601 TTGCTTACACATGCTGCTTATCAAAACGCGATCCGCAACACTGGAAGAACACAAAT 660
    |||||||
DB 601 TTGCTTACACATGCTGCTTATCAAAACGCGATCCGCAACACTGGAAGAACACAAAT 660
OY 661 CGGAGCTGCGACACTTCATGACACTGGAACAAATGAAAGGAGCTACGAACGACGA 720
    |||||||
DB 661 CGGAGCTGCGACACTTCATGACACTGGAACAAATGAAAGGAGCTACGAACGACGA 720
OY 721 GAAAGTGAAGAAAGTGGAGCGCGGAGAGCAAGACAGAGGTTGATGATTTGGCGTGA 780
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DB 721 GAAAGTGAAGAAAGTGGAGCGCGGAGAGCAAGACAGAGGTTGATGATTTGGCGTGA 780
OY 781 GTAACAGCTGAGGACCTTGAATGATGAGTGTGCTGTGTGGCGGATGATGATTCAGC 840
    |||||||
DB 781 GTAACAGCTGAGGACCTTGAATGATGAGTGTGCTGTGTGGCGGATGATGATTCAGC 840
OY 841 TTTGAAGTAACTGATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTA 900
    |||||||
DB 841 TTTGAAGTAACTGATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTA 900
OY 901 ATCTCATTTTTCCTCAGATGATTCCTCATCTTGAACCTGGAAGAGTGGAAAGCTAGG 960
    |||||||
DB 901 ATCTCATTTTTCCTCAGATGATTCCTCATCTTGAACCTGGAAGAGTGGAAAGCTAGG 960
OY 961 CCACAAATTAAGGCTCTCTGTGTGATTTAGATTTTCTGCAATTTTTCGATTGGCT 1020
    |||||||
DB 961 CCACAAATTAAGGCTCTCTGTGTGATTTAGATTTTCTGCAATTTTTCGATTGGCT 1020
OY 1021 TTTTGTGCGCAAAACCTACTTCCGCGTAAATATCAACTTTTCCGTGTTGATATTTC 1080
    |||||||
DB 1021 TTTTGTGCGCAAAACCTACTTCCGCGTAAATATCAACTTTTCCGTGTTGATATTTC 1080
OY 1081 GTCAAAACCCCTGAACCTTAATTTTCTGCGCGGCTAGCCTCCGCTCTCTTCCA 1140
    |||||||
DB 1081 GTCAAAACCCCTGAACCTTAATTTTCTGCGCGGCTAGCCTCCGCTCTCTTCCA 1140
OY 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTA 1200
    |||||||
DB 1141 CATTTCCAAAGTACCCCTGATCTCAATTAATTAATTAATTAATTAATTAATTAATTA 1200
OY 1201 GTGGCCCTTCCAACTCCCAAAATTCGTGACGCTAGCGACCTTTGATTAATTTT 1260
    |||||||
DB 1201 GTGGCCCTTCCAACTCCCAAAATTCGTGACGCTAGCGACCTTTGATTAATTTT 1260
OY 1261 TTCAATTTGTTTCTCTCAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1315
    |||||||
DB 1261 TTCAATTTGTTTCTCTCAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1315

```

RESULT 6
US-08-288-295-5
Sequence 5, Application US/08288295

GENERAL INFORMATION:

APPLICANT: Horvitz, H. Robert
 TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: FISH & RICHARDSON
 STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A. (F) ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/288,295
 FILING DATE: 10-AUG-1994
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/927,681
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 01997/201003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1315 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE: CDNA to mRNA
 NAME/KEY: CDS
 LOCATION: 7..846
 OTHER INFORMATION: /product= "Ced-9"

US-08-288-295-5

Query Match 99.8%; Score 1313; DB 6; Length 1315;
 Best Local Similarity 99.9%; Pred. No. 3.5e-288;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 TTTGATGATGACGCTGCGAGCGGAGACACTCGCTGACGAAATCCGGCGTATCGGCGAGCA 60
D 1 TTTGATGATGACGCTGCGAGCGGAGACACTCGCTGACGAAATCCGGCGTATCGGCGAGCA 60
QY 61 ACGATGCGACGTGGCGAGATGAAGAGCTTTCTGGGATAAAGCGACAGCCACCGAT 120
D 61 ACGATGCGACGTGGCGAGATGAAGAGCTTTCTGGGATAAAGCGACAGCCACCGAT 120
QY 121 TTTGATGATGATGATGCTGCTGAGGACTTCCCATCACCGAGTAGAGAGCTTTCAGCGCA 180
D 121 TTTGATGATGATGATGCTGCTGAGGACTTCCCATCACCGAGTAGAGAGCTTTCAGCGCA 180
QY 181 AGAATGTCATCGGAGAGTCATTTGATGAGAAAATCAATGATGGGAGAGCCAAAGGCTT 240
D 181 AGAATGTCATCGGAGAGTCATTTGATGAGAAAATCAATGATGGGAGAGCCAAAGGCTT 240
QY 241 GATATGAGGAGATTGGTGGCTGATTTTCAGCGACCGGATCCGGCAAAACGGAATGGAA 300
D 241 GATATGAGGAGATTGGTGGCTGATTTTCAGCGACCGGATCCGGCAAAACGGAATGGAA 300
QY 301 TCGTTTGACACCGGAGATTGCGTGTGAGTAGCAACCGGACGACGAATGATGGAGATT 360
D 301 TCGTTTGACACCGGAGATTGCGTGTGAGTAGCAACCGGACGACGAATGATGGAGATT 360

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D 301 TCGTTTGACACCGGAGATTGCGTGTGAGTAGCAACCGGACGACGAATGATGGAGATT 360
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D 361 ATGGAGCATATTCGAGAAAGACAGCGGAAAATTTGAGACTTGTGAGAGAGCTG 420
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QY 541 GGTTCGTACCTGCAAAAATGATGAAATCCGTGGAACTCAGGAGCAAGTGGAAACCTC 600
D 541 GGTTCGTACCTGCAAAAATGATGAAATCCGTGGAACTCAGGAGCAAGTGGAAACCTC 600
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D 601 TTTGTTTACATCGCTGTTCATCAAAAACCGGATCCGCAACACTGGAAGAACACAT 660
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D 661 CGGAGCTGGGAGAGCTTTCATGACACTCGGAAAACAAATGAAAGAGAGCTACGAAAGCA 720
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D 721 GAAGCTGAAAAAGTGGAGACCGGAGAGCAAGAACAGAGCGTGTGATGATGGCGCTGA 780
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D 781 GTAACAGCTGGAGCCATTTGGAATCCTTGAGTCTGTGTGGCGGAGATGATTTGAGC 840
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D 841 TTGAAGTAACTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
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D 901 ATCTATTTTGGCTCAGTATGATCTCATCTTGAACCTGGAAGAGTGGGAAGCTAGG 960
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D 961 CCACAAATTTAGGCTCTCTGCTGATGATTTAGATTTTACGCAATTTTTCGATTTGCT 1020
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D 1021 TTTTGTGGCCAAACCTCTACCTCCGGTAAATCAACTTTTCCGTTCTGTACATTTTC 1080
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D 1081 GTCAAAAACCTGAAACCTTAATTTTCTGCGCGTGGCTAGCTCCGCTTCTCTTCCA 1140
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D 1141 CATTTCAAAAGTACCCCTGTATCTCAATATTAATTAATTAATTAATTAATTAATTAAT 1200
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D 1201 GTGGCTCTTCCAAATCCCTGCAATTTCTGTAACGCTGACGCTGCTGCTTCTTCT 1260
QY 1261 TTCAAATTTTCTCTCTACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1315
D 1261 TTCAAATTTTCTCTCTACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1315

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RESULT 7

US-08-288-295-6
 Sequence 6, Application US/08288295
 GENERAL INFORMATION:
 APPLICANT: Horvitz, H. Robert
 APPLICANT: Hengartner, Michael

TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
 CELL DEATH AND USES THEREFOR
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: FISH & RICHARDSON
 STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A. (F) ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.0
 CURRENT APPLICATION DATA: US/08/288,295
 APPLICATION NUMBER: US/08/288,295
 FILING DATE: 10-AUG-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/927,681
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 01997/201003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1315 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..846
 OTHER INFORMATION: /product= "Ced-9"
 US-08-288-295-6

Query Match 99.8%; Score 1313; DB 6; Length 1315;
 Best Local Similarity 99.9%; Pired. No. 3.5e-288;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGATGACAGCTGACAGCGGACGACACTGCTGACGATCCGGCGTATCGGCGACGA 60
 DB 1 TTGAGATGACAGCTGACAGCGGACGACACTGCTGACGATCCGGCGTATCGGCGACGA 60
 QY 61 ACGATGCGGACGTCGAGATGAGAGAGTTTCTGGGGATMAAAGGCAAGAGCCACCGAT 120
 DB 61 ACGATGCGGACGTCGAGATGAGAGAGTTTCTGGGGATMAAAGGCAAGAGCCACCGAT 120
 QY 121 TTTGGAATCAATGATGATGCTCAGAGCTTGCATCAGGAGTAGACGAGCTTCAGCAGCA 180
 DB 121 TTTGGAATCAATGATGATGCTCAGAGCTTGCATCAGGAGTAGACGAGCTTCAGCAGCA 180
 QY 121 TTTGGAATCAATGATGATGCTCAGAGCTTGCATCAGGAGTAGACGAGCTTCAGCAGCA 180
 DB 121 TTTGGAATCAATGATGATGCTCAGAGCTTGCATCAGGAGTAGACGAGCTTCAGCAGCA 180
 QY 181 AGAATGTCATCGAGAGTCAATGATGAGAAATCAATGATGAGAAATCAATGATGAGAAAT 240
 DB 181 AGAATGTCATCGAGAGTCAATGATGAGAAATCAATGATGAGAAATCAATGATGAGAAAT 240
 QY 241 GATATCGAGGATTTGTGTGATGATTTCAACGACGATCCGCAAAAGGAAATGGA 300
 DB 241 GATATCGAGGATTTGTGTGATGATTTCAACGACGATCCGCAAAAGGAAATGGA 300
 QY 301 TGGTTGGAGACGCGGAGATGCGGTGTGAGATGCAACCGGAGACGAAATGATGAGATT 360
 DB 301 TGGTTGGAGACGCGGAGATGCGGTGTGAGATGCAACCGGAGACGAAATGATGAGATT 360
 QY 361 ATGGAGAGATATTCGAGAGAGACGCGGAAATTTTGGAGACTTCTGTGAGCAGCTG 420

DB 361 ATGGAGAGATATTCGAGAGAGACGCGGAAATTTTGGAGACTTCTGTGAGCAGCTG 420
 QY 421 CTCGAGTCCCGAGAGATTCATTTTACTGATATCGAGATGCTGCGAGCGTTGGAAT 480
 DB 421 CTCGAGTCCCGAGAGATTCATTTTACTGATATCGAGATGCTGCGAGCGTTGGAAT 480
 QY 481 GCACAGACAGATCAATGCTCAATGCTTATGAACTGTTATGATGCTTATGCTTCTG 540
 DB 481 GCACAGACAGATCAATGCTCAATGCTTATGAACTGTTATGATGCTTATGCTTCTG 540
 QY 541 GATTTCGAGTCCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
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 QY 601 TTTGTTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 DB 601 TTTGTTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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 DB 661 CGGAGCTGGAGACATTCATGACACTCGGAAACAAATGAAAGAGACTACGAAAGAGCA 720
 QY 721 GAAGCTGAAAGATGGAGACCGCGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 721 GAAGCTGAAAGATGGAGACCGCGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 QY 781 GTACAGCTGGAGACATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 DB 781 GTACAGCTGGAGACATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 840
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 DB 841 TTGAAGTACGATTCATTTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
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 DB 901 ATCTCATTTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
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 DB 1021 TTTTTCGCGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 QY 1081 GTCAAAACCTGGAACCTTAATTTTCTGCGCGTGTGCTGCTGCTGCTGCTGCTGCTG 1140
 DB 1081 GTCAAAACCTGGAACCTTAATTTTCTGCGCGTGTGCTGCTGCTGCTGCTGCTGCTG 1140
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 DB 1141 CATTTCCAAAGTACCGCTGATTCATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
 QY 1201 GTGGCTTTCGCAACTCCGCAAAATTCCTGATGAGCGTACGCGACTTGTATTTT 1260
 DB 1201 GTGGCTTTCGCAACTCCGCAAAATTCCTGATGAGCGTACGCGACTTGTATTTT 1260
 QY 1261 TTCAAAATGTTTCTCTGATCAACAAACAAACAAACAAACAAACAAACAAACAAAC 1315
 DB 1261 TTCAAAATGTTTCTCTGATCAACAAACAAACAAACAAACAAACAAACAAACAAAC 1315

RESULT 8
 US-08-801-248-4
 Sequence 4, Application US/08801248
 GENERAL INFORMATION:
 APPLICANT: Horvitz, H. Robert
 APPLICANT: Hengartner, Michael
 TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
 TITLE OF INVENTION: CELL DEATH AND USES THEREFOR

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: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FISH & RICHARDSON
: STREET: 225 Franklin Street, Suite 3100
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Wordperfect 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/801,248
: FILING DATE: 19-FEB-1997
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/288,295
: FILING DATE: 10-AUG-1994
: APPLICATION NUMBER: US 07/927,681
: FILING DATE: 10-AUG-1992
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,162
: REFERENCE/DOCKET NUMBER: 01997/201003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-5070
: TELEFAX: (617) 542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1315 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 7..846
: OTHER INFORMATION: /product= "Ced-9"
: US-08-801-248-4

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Query Match 99.8%; Score 1313; DB 12; Length 1315;
 Best Local Similarity 99.9%; Pred. No. 3.5e-288;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 ACGATGGCGAGTGGCGAGATGAAGAGTTCTGTGGGATAAAGAGCAGAGAGCCACCGAT 120
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Db 61 ACGATGGCGAGTGGCGAGATGAAGAGTTCTGTGGGATAAAGAGCAGAGAGCCACCGAT 120
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QY 181 AGAATGTCATCGGAGAGTCAATTGATGAAAAATCAATGATTGGGAAGAGCCAGGCTT 240
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Db 181 AGAATGTCATCGGAGAGTCAATTGATGAAAAATCAATGATTGGGAAGAGCCAGGCTT 240
QY 241 GATATCGAGGAGATTGTGTGCTGACTATTTCAGCGACCGGAATCCGGGCAAAAACGGAAATGGAA 300
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Db 241 GATATCGAGGAGATTGTGTGCTGACTATTTCAGCGACCGGAATCCGGGCAAAAACGGAAATGGAA 300
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Db 301 TGGTTTGGACACCGGAGATTGCGGTGTGAGTGAACCGGAGAGCAAAATGATGCGAGTT 360
QY 361 ATGGGAACGATATTTCGAGAAAGAACACGCGGAAATTTTCAGACCTTCTGTGAGCAGCTG 420

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Db 361 ATGGGAACGATATTTCGAGAAAGAACACGCGGAAATTTTGAGACCTTCTGTGAGCAGCTG 420
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Db 421 CTCGAGTGGCCAGATCTCATTTTCTCATGTATCAGATGTGTGTTCCGAGCGTTGGAAT 480
QY 481 GCACAGACAGATCATGTCTATGCTATGAGAGTGTGATGAGGCTTAATCTGCTGGC 540
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Db 661 CGGAGCTGGGACGACTTCATGACACTCGGAAACAAATGAAAGAGACTACGAACGAGCA 720
QY 721 GAAGCTGAAAAAGTGGAGCGCCGGAACAGACAGAGCGTGTGATGATTGCGCTGGA 780
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Db 721 GAAGCTGAAAAAGTGGAGCGCCGGAACAGACAGAGCGTGTGATGATTGCGCTGGA 780
QY 781 GTAACAGCTGGAGCATTGGAATGCTGGAGTGTGCTGTGTTGGGAGATGATGTTCCAG 840
   |||||||
Db 781 GTAACAGCTGGAGCATTGGAATGCTGGAGTGTGCTGTGTTGGGAGATGATGTTCCAG 840
QY 841 TTGAAGTAAAGCTATTCATTTTGTAAATTAATTAATTAATTAATTAATTAATTAATTA 900
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Db 841 TTGAAGTAAAGCTATTCATTTTGTAAATTAATTAATTAATTAATTAATTAATTAATTA 900
QY 901 ATCTCATTTTGGCTCACTGATCTGTCATCCTTGAACGGAAGAGAGTGGAAAGTAG 960
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Db 901 ATCTCATTTTGGCTCACTGATCTGTCATCCTTGAACGGAAGAGAGTGGAAAGTAG 960
QY 961 CCAACAAATTAAGGCTCTGCTGTGATGATTAACGATTTTACTGCAATTTTCCGATGCT 1020
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QY 1021 TTTTGTGGCGAAACCCCTACTTCCCGGTAATATCAACTTTTCGTTCTGTACATTTTC 1080
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Db 1021 TTTTGTGGCGAAACCCCTACTTCCCGGTAATATCAACTTTTCGTTCTGTACATTTTC 1080
QY 1081 GTCAAAAACCCCTGAACCCCTAATTTTCTGCGCGTGGCTAGCCTCCGCTTCTTCCA 1140
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Db 1081 GTCAAAAACCCCTGAACCCCTAATTTTCTGCGCGTGGCTAGCCTCCGCTTCTTCCA 1140
QY 1141 CATTTCGAAGTACCCCTGATCTCAATTAATTCATCTTCACTTAAGTGTCTTTTGT 1200
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Db 1141 CATTTCGAAGTACCCCTGATCTCAATTAATTCATCTTCACTTAAGTGTCTTTTGT 1200
QY 1201 GTGGCCTCTTCAACCTCCCGCAAAATCTCTGACGAGTACCGGAGCTTGTATTTT 1260
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Db 1201 GTGGCCTCTTCAACCTCCCGCAAAATCTCTGACGAGTACCGGAGCTTGTATTTT 1260
QY 1261 TTCAATTTTCTTCTCTACAAACAAAAAAGGTTCAAAAAAAGGTTCAAAAAAAGGTT 1315
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Db 1261 TTCAATTTTCTTCTCTACAAACAAAAAAGGTTCAAAAAAAGGTTCAAAAAAAGGTT 1315

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RESULT 9
 US-08-801-248-5
 Sequence 5, Application US/08801248
 GENERAL INFORMATION:
 APPLICANT: Horvitz, H. Robert
 APPLICANT: Hengartner, Michael
 TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
 TITLE OF INVENTION: CELL DEATH AND USES THEREFOR

NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & RICHARDSON
 STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,248
 FILING DATE: 19-FEB-1997
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/288,295
 FILING DATE: 10-AUG-1994
 APPLICATION NUMBER: US 07/927,681
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 01997/201003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ. ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1315 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..846
 OTHER INFORMATION: /product= "Ced-9"
 US-08-801-248-5

Query Match 99.8%; Score 1313; DB 12; Length 1315;
 Best Local Similarity 99.9%; Pred. No. 3.5e-288;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 1 TTTGAGATGACACGCTGACGCGGACGACACTGCTGACGAAATCCGGCGTATGCGCGACGA 60
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 61 ACGATGGCGAGCTGGCGAGATGAAAGAGTTCTGCGGATTAAGGACAGAGCCACCGAT 120
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 361 ATGGACGATATTTGAGAGAGACGCGGAAAAATTTTGAGACCTTCTGTGAGACAGCTG 420

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 1021 TTTTGTGGGCAAAACCTCTATCTCGGCTAATATCAATTTTCCGTTCTGTACATTTTC 1080
 1021 TTTTGTGGGCAAAACCTCTATCTCGGCTAATATCAATTTTCCGTTCTGTACATTTTC 1080
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 1261 TTCAAAATGTTTCTCTACCAACCAAAAAAAGGTTCAAAAAAAGGTTCAAAAAA 1315

RESULT 10
 US-08-801-248-6
 ; Sequence 6, Application US/08801248
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, H. Robert
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
 ; TITLE OF INVENTION: CELL DEATH AND USES THEREFOR

```

; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Nordperfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,248
; FILING DATE: 19-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/288,295
; FILING DATE: 10-AUG-1994
; APPLICATION NUMBER: US 07/927,681
; FILING DATE: 10-AUG-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 01997/201003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1315 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..846
; OTHER INFORMATION: /product="Ced-9"
; US-08-801-248-6

```

Query Match 99.8%; Score 1313; DB 12; Length 1315;
 Best Local Similarity 99.98%; Pred. No. 3.5e-288;
 Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 TTGAGATGACACGCTGACGCGGACAACTGCTGACGAAATCCGGGCTATCGGCGACGA 60
D 1 TTGAGATGACACGCTGACGCGGACAACTGCTGACGAAATCCGGGCTATCGGCGACGA 60
QY 61 ACGATGGGACTGCGGAGATGAGAGAGTTTCTGGGATTAAGGACACAGACCCACCGAT 120
D 61 ACGATGGGACTGCGGAGATGAGAGAGTTTCTGGGATTAAGGACACAGACCCACCGAT 120
QY 121 TTGGAATCAATAGTATGATGCTCAGGACTTGCATACCGAGATAGGAGGCTTCAGCGCA 180
D 121 TTGGAATCAATAGTATGATGCTCAGGACTTGCATACCGAGATAGGAGGCTTCAGCGCA 180
QY 181 AGAATGTCATCGAGAGTCAATTGATGAGAAAAATCATGATGATGGAGAGCCAAAGCTT 240
D 181 AGAATGTCATCGAGAGTCAATTGATGAGAAAAATCATGATGATGGAGAGCCAAAGCTT 240
QY 241 GATATCGAGGATTTGGTGTGACTATTTTCAACGACGAATCCGGCAAAAACGGAATGAA 300
D 241 GATATCGAGGATTTGGTGTGACTATTTTCAACGACGAATCCGGCAAAAACGGAATGAA 300
QY 301 TGGTTTGAGACCCGGGATTCCTGTGAGATGCAACCGGAGCAAGAAATGATCCGAGTT 360
D 301 TGGTTTGAGACCCGGGATTCCTGTGAGATGCAACCGGAGCAAGAAATGATCCGAGTT 360
QY 361 ATGGGAACGATATTCGAGAAAGAACACGCGGAAAAATTTTGAAGACCTTCTGTGACAGCTG 420

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D 361 ATGGGAACGATATTCGAGAAAGAACACGCGGAAAAATTTTGAAGACCTTCTGTGACAGCTG 420
QY 421 CTCGCGATGCCGAGAAATCATTTTCACTGTATCAGAGATGTGTTGGACGGTTGGAAT 480
D 421 CTCGCGATGCCGAGAAATCATTTTCACTGTATCAGAGATGTGTTGGACGGTTGGAAT 480
QY 481 GCACAGACGATCAATGTCATATGCTTATGAGACGTTGATAGTCTATCTCGTTGGC 540
D 481 GCACAGACGATCAATGTCATATGCTTATGAGACGTTGATAGTCTATCTCGTTGGC 540
QY 541 GGTTCGTAGCTGCAAAAATGATGAAATCCGTGGAATCTGACAGGACAAAGTCCGAACCTC 600
D 541 GGTTCGTAGCTGCAAAAATGATGAAATCCGTGGAATCCGTGGAATCTGACAGGACAAACCTC 600
QY 601 TTCGTTTACATCGCTGTTATCATCAAAACGGGAGATCCGCAACACTGGAAAGAACACAT 660
D 601 TTCGTTTACATCGCTGTTATCATCAAAACGGGAGATCCGCAACACTGGAAAGAACACAT 660
QY 661 CGGAGCTGGACGACTTATGACACTCGGAAACAAATGAAAGAGACTACGAAACGAGCA 720
D 661 CGGAGCTGGACGACTTATGACACTCGGAAACAAATGAAAGAGACTACGAAACGAGCA 720
QY 721 GAAGCTGAAAAAGTGGGACGCGGAGAGACAGACGAGGTGATGATTTGCGCTGGA 780
D 721 GAAGCTGAAAAAGTGGGACGCGGAGAGACAGACGAGGTGATGATTTGCGCTGGA 780
QY 781 GTACAGCTGAGCCATTTGGAATCGTTGAGATCGCTGTTGTTGGCGGATGATGTTGAGC 840
D 781 GTACAGCTGAGCCATTTGGAATCGTTGAGATCGCTGTTGTTGGCGGATGATGTTGAGC 840
QY 841 TTGAAGTACGATTTCAATTTGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
D 841 TTGAAGTACGATTTCAATTTGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
QY 901 ATCTCAATTTTGGCTCAGTATTTCTCATCTTTGAACTGGAGAGAGTGGGAAAGCTAGG 960
D 901 ATCTCAATTTTGGCTCAGTATTTCTCATCTTTGAACTGGAGAGAGTGGGAAAGCTAGG 960
QY 961 CCACAAATTCAGGCTCTCTGTGATTTGATGATTTTACTGCAATTTTCCGATTGGCT 1020
D 961 CCACAAATTCAGGCTCTCTGTGATTTGATGATTTTACTGCAATTTTCCGATTGGCT 1020
QY 1021 TTTTGTGGCAAAACCTTCTCCGCTAATTCACACTTTTCGTTCTGTACATTTTC 1080
D 1021 TTTTGTGGCAAAACCTTCTCCGCTAATTCACACTTTTCGTTCTGTACATTTTC 1080
QY 1081 GTCAAAAACCTGAAACCTTAATTTTCTGCGGCTAGGCTCCGCTTCTCTTCCA 1140
D 1081 GTCAAAAACCTGAAACCTTAATTTTCTGCGGCTAGGCTCCGCTTCTCTTCCA 1140
QY 1141 CATTCCAAAGTACCCCTGATCTCAATTAATTAATTTTCACTTCACTTCTCTTTCGT 1200
D 1141 CATTCCAAAGTACCCCTGATCTCAATTAATTAATTTTCACTTCACTTCTCTTTCGT 1200
QY 1201 GTGGCCTTCCCAACCTCCGCAAAATTCCTGTACGCGTACGCGACTTGTATTTATTTT 1260
D 1201 GTGGCCTTCCCAACCTCCGCAAAATTCCTGTACGCGTACGCGACTTGTATTTATTTT 1260
QY 1261 TTTCAATTTGTTTCTGTACCAACAACAAAAAAGTTTCAAAAAAAGTTTCAAAAAAAGTTT 1315
D 1261 TTTCAATTTGTTTCTGTACCAACAACAAAAAAGTTTCAAAAAAAGTTTCAAAAAAAGTTT 1315

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RESULT 11
 US-09-993-420a-4
 ; Sequence 4, Application US/09993420A
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, H. Robert
 ; APPLICANT: Hengartner, Michael
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
 ; TITLE OF INVENTION: USES THEREOF

```

FILE REFERENCE: 01997/201006
CURRENT APPLICATION NUMBER: US/09/993,420A
CURRENT FILING DATE: 5001-11-09
PRIOR APPLICATION NUMBER: 09/234,186
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: 07/898,933
PRIOR FILING DATE: 1992-06-12
PRIOR APPLICATION NUMBER: 07/927,681
PRIOR FILING DATE: 1992-08-10
PRIOR APPLICATION NUMBER: 08/288,295
PRIOR FILING DATE: 1994-08-10
PRIOR APPLICATION NUMBER: 08/801,248
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1315
TYPE: DNA
ORGANISM: Caenorhabditis elegans
FEATURE:
NAME/KEY: CDS
LOCATION: (7)...(846)
US-09-993-420A-4

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Query Match          99.8%; Score 1313; DB 37; Length 1315;
Best Local Similarity 99.9%; Pred. No. 3.5e-288;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 TTTGAGATGACACGCTCCACGCGGACACACTCGCTGACGATCCGGCGTATGCGGCGCA 60
D 1 TTTGAGATGACACGCTCCACGCGGACACACTCGCTGACGATCCGGCGTATGCGGCGCA 60
QY 61 ACGATGCGGCGGCGGCGGATGCAAGAGCTTTGCGGTAAGAGGACAGAGCCACCGAT 120
D 61 ACGATGCGGCGGCGGCGGATGCAAGAGCTTTGCGGTAAGAGGACAGAGCCACCGAT 120
QY 121 TTTGGAATCAATAGTGTGCTCAGAGCTTGGCCATCACCGAGTAGGAGGCTTTCAGCGCA 180
D 121 TTTGGAATCAATAGTGTGCTCAGAGCTTGGCCATCACCGAGTAGGAGGCTTTCAGCGCA 180
QY 121 TTTGGAATCAATAGTGTGCTCAGAGCTTGGCCATCACCGAGTAGGAGGCTTTCAGCGCA 180
D 121 TTTGGAATCAATAGTGTGCTCAGAGCTTGGCCATCACCGAGTAGGAGGCTTTCAGCGCA 180
QY 181 AGAATGTCATCGAGAGCTCAATGATGGAAGAAATCAATGATTTGGGAAGGCCAAGGCTT 240
D 181 AGAATGTCATCGAGAGCTCAATGATGGAAGAAATCAATGATTTGGGAAGGCCAAGGCTT 240
QY 181 AGAATGTCATCGAGAGCTCAATGATGGAAGAAATCAATGATTTGGGAAGGCCAAGGCTT 240
D 181 AGAATGTCATCGAGAGCTCAATGATGGAAGAAATCAATGATTTGGGAAGGCCAAGGCTT 240
QY 241 GATATCGAGGAGTTGGTGACATTTTCACGACCGAATCCGGCAAAACGGAATGGA 300
D 241 GATATCGAGGAGTTGGTGACATTTTCACGACCGAATCCGGCAAAACGGAATGGA 300
QY 241 GATATCGAGGAGTTGGTGACATTTTCACGACCGAATCCGGCAAAACGGAATGGA 300
D 241 GATATCGAGGAGTTGGTGACATTTTCACGACCGAATCCGGCAAAACGGAATGGA 300
QY 301 TGGTTTGAGAGACCGGAGATTCGCTGTGAGTGCACACCGAGACGAATGATCGAGTT 360
D 301 TGGTTTGAGAGACCGGAGATTCGCTGTGAGTGCACACCGAGAGCAATGATCGAGTT 360
QY 301 TGGTTTGAGAGACCGGAGATTCGCTGTGAGTGCACACCGAGAGCAATGATCGAGTT 360
D 301 TGGTTTGAGAGACCGGAGATTCGCTGTGAGTGCACACCGAGAGCAATGATCGAGTT 360
QY 361 ATGGAGACGATATTCGAGAGAGAGACCGGGAATTTTGGACCTTCTTGAGAGAGTGTG 420
D 361 ATGGAGACGATATTCGAGAGAGAGACCGGGAATTTTGGACCTTCTTGAGAGAGTGTG 420
QY 361 ATGGAGACGATATTCGAGAGAGAGACCGGGAATTTTGGACCTTCTTGAGAGAGTGTG 420
D 361 ATGGAGACGATATTCGAGAGAGAGACCGGGAATTTTGGACCTTCTTGAGAGAGTGTG 420
QY 421 CTGCGAGTCCGAGATTCATTTTCATCTGATCAGATGATGATGATGATGATGATGATGAT 480
D 421 CTGCGAGTCCGAGATTCATTTTCATCTGATCAGATGATGATGATGATGATGATGATGAT 480
QY 421 CTGCGAGTCCGAGATTCATTTTCATCTGATCAGATGATGATGATGATGATGATGATGAT 480
D 421 CTGCGAGTCCGAGATTCATTTTCATCTGATCAGATGATGATGATGATGATGATGATGAT 480
QY 481 GCACAGACGATCAATGTCATGCTTCTATGAGAGCTTTGATGATGATGATGATGATGATGAT 540
D 481 GCACAGACGATCAATGTCATGCTTCTATGAGAGCTTTGATGATGATGATGATGATGATGAT 540
QY 481 GCACAGACGATCAATGTCATGCTTCTATGAGAGCTTTGATGATGATGATGATGATGATGAT 540
D 481 GCACAGACGATCAATGTCATGCTTCTATGAGAGCTTTGATGATGATGATGATGATGATGAT 540
QY 541 GGTTCGTGATGCTGCAAAATGATGATTCCTGAGAACTGCGAGGAGCAAGTGGAAACCTC 600
D 541 GGTTCGTGATGCTGCAAAATGATGATTCCTGAGAACTGCGAGGAGCAAGTGGAAACCTC 600
QY 541 GGTTCGTGATGCTGCAAAATGATGATTCCTGAGAACTGCGAGGAGCAAGTGGAAACCTC 600
D 541 GGTTCGTGATGCTGCAAAATGATGATTCCTGAGAACTGCGAGGAGCAAGTGGAAACCTC 600
QY 601 TTGCTTTACACATCGCTGTTCATCAAAACGCGATCCGCAAACTGAGAGAGACACAT 660
D 601 TTGCTTTACACATCGCTGTTCATCAAAACGCGATCCGCAAACTGAGAGAGACACAT 660
QY 661 CGGAGCTGGAGACTTTCATGACACTCGGAAAAAATGAAAGAGACTTACGACAGAGCA 720

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D 661 CGGAGCTGGAGACTTTCATGACACTCGGAAAAAATGAAAGAGACTTACGACAGAGCA 720
QY 721 GAACCTGAAAAATGAGGAGCGCGGAGACAGAGAGAGGCTGATGATGCGCTGCA 780
D 721 GAACCTGAAAAATGAGGAGCGCGGAGACAGAGAGAGGCTGATGATGCGCTGCA 780
QY 781 GTACAGCTGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
D 781 GTACAGCTGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TTGAAGTACGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
D 841 TTGAAGTACGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 ATTCATTTTGGCTCAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
D 901 ATTCATTTTGGCTCAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 CCACAAATTTAGCGCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
D 961 CCACAAATTTAGCGCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 TTTTGTGGCCAAACCTTACCTTCCGCTAATATCACTTTCCGCTGATGATGATGATGATGAT 1080
D 1021 TTTTGTGGCCAAACCTTACCTTCCGCTAATATCACTTTCCGCTGATGATGATGATGATGAT 1080
QY 1081 GTCAAAACCCCTGAACCCCTTACCTTCCGCTGATGATGATGATGATGATGATGATGATGAT 1140
D 1081 GTCAAAACCCCTGAACCCCTTACCTTCCGCTGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 CATTTCCAAAGTACCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
D 1141 CATTTCCAAAGTACCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 GTGGCCTCTTCCACCTCCGCTAATATCACTTTCCGCTGATGATGATGATGATGATGATGAT 1260
D 1201 GTGGCCTCTTCCACCTCCGCTAATATCACTTTCCGCTGATGATGATGATGATGATGATGAT 1260
QY 1261 TTTCAATTTTCTTCTCTACACAAACAAAAACGTTCAAAAAA 1315
D 1261 TTTCAATTTTCTTCTCTACACAAACAAAAACGTTCAAAAAA 1315

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RESULT 12
US-09-993-420A-5
; Sequence 5, Application US/09993420A
; GENERAL INFORMATION:
; APPLICANT: Hengartner, H. Robert
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 01997/201006
; CURRENT APPLICATION NUMBER: US/09/993,420A
; CURRENT FILING DATE: 5001-11-09
; PRIOR APPLICATION NUMBER: 09/234,186
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:

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NAME/KEY: CDS
LOCATION: (77)...(846)
US-09-993-420a-5

Query Match 99.8%; Score 1313; DB 37; Length 1315;
Best Local Similarity 99.9%; Pred. No. 3.5e-288;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 TTTGAGATGACAGCTGACGAGGCGGACAACTGCTGACGAATCCGGCGATATGCGGACGA 60
DB 1 TTTGAGATGACAGCTGACGAGGCGGACAACTGCTGACGAATCCGGCGATATGCGGACGA 60
QY 61 ACATGCGGAGCTGCGGAGATGAGAGATTCTGGGATAAAGGACAGAGCCACCGAT 120
DB 61 ACATGCGGAGCTGCGGAGATGAGAGATTCTGGGATAAAGGACAGAGCCACCGAT 120
QY 121 TTTGGAATCAATAGTATGCTCAGSACTTCCATCCAGTAGAGAGCTTCGACGCGA 180
DB 121 TTTGGAATCAATAGTATGCTCAGSACTTCCATCCAGTAGAGAGCTTCGACGCGA 180
QY 181 AGAATGTCCATCGAGAGTCAATTTGATGAAAAATCAATGATTGGGAAGCCAGCCTT 240
DB 181 AGAATGTCCATCGAGAGTCAATTTGATGAAAAATCAATGATTGGGAAGCCAGCCTT 240
QY 241 GATATGAGGAGATTGTGTGCTGCACTATTTCACGACCGAATCCGGCAAAACGGAATTGGA 300
DB 241 GATATGAGGAGATTGTGTGCTGCACTATTTCACGACCGAATCCGGCAAAACGGAATTGGA 300
QY 301 TGGTTTGGAGCAACCGGATTTGCGTGTGAGTGAACCGGACGACGAAATGATGCGAGTT 360
DB 301 TGGTTTGGAGCAACCGGATTTGCGTGTGAGTGAACCGGACGACGAAATGATGCGAGTT 360
QY 361 ATGGGAACGATATTCGAGAAAGACACGGGAAAAATTTTGAACCTTCTGTGAGCAGCTG 420
DB 361 ATGGGAACGATATTCGAGAAAGACACGGGAAAAATTTTGAACCTTCTGTGAGCAGCTG 420
QY 421 CTCGCGATCCGAGATTCATTTTCACTGATTCAGAGATGTCGTTGCGAGCGTTGGAAT 480
DB 421 CTCGCGATCCGAGATTCATTTTCACTGATTCAGAGATGTCGTTGCGAGCGTTGGAAT 480
QY 481 GCAGACAGCATCAATGTCATGCTTATGAGAGCTTTGATAGTCTATCTGCTTGGC 540
DB 481 GCATGACAGCATCAATGTCATGCTTATGAGAGCTTTGATAGTCTATCTGCTTGGC 540
QY 541 GGTTCGTAAGCTGCAAAAAATGATGGAATCCGTGAACTGACAGGCAAGTGGAAACCTC 600
DB 541 GGTTCGTAAGCTGCAAAAAATGATGGAATCCGTGAACTGACAGGCAAGTGGAAACCTC 600
QY 601 TTCGTTTACATCGCTGTGATCAAAAACGGGATCCGCAACCACTGAAAGCAACAT 660
DB 601 TTCGTTTACATCGCTGTGATCAAAAACGGGATCCGCAACCACTGAAAGCAACAT 660
QY 661 CGGAGCTGGGAGACTTTCATGACACTCGAAAAACAATGAAGAGACTAGCAAGCA 720
DB 661 CGGAGCTGGGAGACTTTCATGACACTCGAAAAACAATGAAGAGACTAGCAAGCA 720
QY 721 GAAGCTGAAAAAGTGGGACCCGGAAGAGACAGAGCTGTGATGATGGCGCTGA 780
DB 721 GAAGCTGAAAAAGTGGGACCCGGAAGAGACAGAGCTGTGATGATGGCGCTGA 780
QY 781 GTAAACAGTGGAGCATTTGGAATGCTGAGTGTGCGTGGGCGGAGATGTTGAGC 840
DB 781 GTAAACAGTGGAGCATTTGGAATGCTGAGTGTGCGTGGGCGGAGATGTTGAGC 840
QY 841 TTGAAGTACGATTTCAATTTGTAAATATTAATTATGATACAACTCCCTTACATTGA 900
DB 841 TTGAAGTACGATTTCAATTTGTAAATATTAATTATGATACAACTCCCTTACATTGA 900
QY 901 ATTCATTTTGTGACGATTTCTCATCTTGAAGTGAAGTGGGAAAGCTAGG 960
DB 901 ATTCATTTTGTGACGATTTCTCATCTTGAAGTGAAGTGGGAAAGCTAGG 960
QY 961 CCACAATTAAGGCTCTCTGTGATTTAGATTTTACTGCAATTTTCCGATTGCTT 1020

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DB 961 CCACAATTAAGGCTCTCTGTGATTTAGATTTTACTGCAATTTTCCGATTGCTT 1020
QY 1021 TTTTGTGGCCAAACCTTACTTCCGGAATATCACTTTCCGTGTCATATTC 1080
DB 1021 TTTTGTGGCCAAACCTTACTTCCGGAATATCACTTTCCGTGTCATATTC 1080
QY 1081 GTCAAAAACCTGAAACCTTAATTTTCTGCGCGTGGGCTAGCCTCCGCTTCTTCCA 1140
DB 1081 GTCAAAAACCTGAAACCTTAATTTTCTGCGCGTGGGCTAGCCTCCGCTTCTTCCA 1140
QY 1141 CATTTCCAAAGTACCCCGTATCTCAATTAATTCATCTTCACTTTATCTTTGCT 1200
DB 1141 CATTTCCAAAGTACCCCGTATCTCAATTAATTCATCTTCACTTTATCTTTGCT 1200
QY 1201 GTGGCTTCTCCAACTCCCGCAATTCCTGTACGCGTACGCGACTTGTATTTATTTT 1260
DB 1201 GTGGCTTCTCCAACTCCCGCAATTCCTGTACGCGTACGCGACTTGTATTTATTTT 1260
QY 1261 TTCAATTTGTTTCTCTTACACACAAAAAAGGTTCAAAAAA 1315
DB 1261 TTCAATTTGTTTCTCTTACACACAAAAAAGGTTCAAAAAA 1315

```

RESULT 13

US-09-993-420a-6

Sequence 6, Application US/09993420A

GENERAL INFORMATION:

APPLICANT: Horvitz, H. Robert

APPLICANT: Hengartner, Michael

TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A

TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND

FILE REFERENCE: US97/201006

CURRENT APPLICATION NUMBER: US/09/993,420A

PRIOR APPLICATION NUMBER: 5001-11-09

PRIOR FILING DATE: 1992-06-12

PRIOR FILING DATE: 1992-08-10

PRIOR FILING DATE: 1994-08-10

PRIOR FILING DATE: 1997-02-19

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 1315

TYPE: DNA

ORGANISM: Caenorhabditis elegans

FEATURE:

NAME/KEY: CDS

LOCATION: (77)...(846)

US-09-993-420a-6

Query Match 99.8%; Score 1313; DB 37; Length 1315;
Best Local Similarity 99.9%; Pred. No. 3.5e-288;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 TTTGAGATGACAGCTGACGAGGCGGACAACTGCTGACGAATCCGGCGATATGCGGACGA 60
DB 1 TTTGAGATGACAGCTGACGAGGCGGACAACTGCTGACGAATCCGGCGATATGCGGACGA 60
QY 61 ACATGCGGAGCTGCGGAGATGAGAGATTCTGGGATAAAGGACAGAGCCACCGAT 120
DB 61 ACATGCGGAGCTGCGGAGATGAGAGATTCTGGGATAAAGGACAGAGCCACCGAT 120
QY 121 TTTGGAATCAATAGTATGCTCAGSACTTCCATCCAGTAGAGAGCTTCGACGCGA 180
DB 121 TTTGGAATCAATAGTATGCTCAGSACTTCCATCCAGTAGAGAGCTTCGACGCGA 180

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QY 181 AGAATGTCATCGAGAGTCATTTGATGAAAAATCAATGATTGGAGAGCCAGGCTT 240
 DB 181 AGAATGTCATCGAGAGTCATTTGATGAAAAATCAATGATTGGAGAGCCAGGCTT 240
 QY 241 GATATGAGGAGTATTTGGTGCAGCTATTTCCAGCCAGATCCGGGAAAAAGGAAATGGA 300
 DB 241 GATATGAGGAGTATTTGGTGCAGCTATTTCCAGCCAGATCCGGGAAAAAGGAAATGGA 300
 QY 301 TGGTTTGGACACCGGAGTGGCGTGTGAGTCAACCGGAGCAGCAAAATGATGCGAGTT 360
 DB 301 TGGTTTGGACACCGGAGTGGCGTGTGAGTCAACCGGAGCAGCAAAATGATGCGAGTT 360
 QY 361 ATGGGAACGATTTTCGAGAAAGACGCGGAAAAATTTTGAACCTTCTGTGAGCAGCTG 420
 DB 361 ATGGGAACGATTTTCGAGAAAGACGCGGAAAAATTTTGAACCTTCTGTGAGCAGCTG 420
 QY 421 CTGCGACATGGCCAGAAATCTATTTTCATCTGATCAGGATGGTTGGAGGATTTGGAAT 480
 DB 421 CTGCGACATGGCCAGAAATCTATTTTCATCTGATCAGGATGGTTGGAGGATTTGGAAT 480
 QY 481 GCACAGACAGATCAATGTCATGCTTATGAGAGCTTTGATGAGTCTATCTGCTGGC 540
 DB 481 GCACAGACAGATCAATGTCATGCTTATGAGAGCTTTGATGAGTCTATCTGCTGGC 540
 QY 541 GGTTCGTAGCTGAAAAATGATGGAATCGTGGACTGCAAGGACAAAGTCCGAAACCTC 600
 DB 541 GGTTCGTAGCTGAAAAATGATGGAATCGTGGACTGCAAGGACAAAGTCCGAAACCTC 600
 QY 601 TTGCTTTACACATGCTGTTTCATCAAAAACGGGATCCGCAACAATGGAAGAACACAT 660
 DB 601 TTGCTTTACACATGCTGTTTCATCAAAAACGGGATCCGCAACAATGGAAGAACACAT 660
 QY 661 CGAGAGCTGGGACGACTTCATGACCTGCGAAAAACAATGAAAGGAGCTCGAAGCGAGCA 720
 DB 661 CGAGAGCTGGGACGACTTCATGACCTGCGAAAAACAATGAAAGGAGCTCGAAGCGAGCA 720
 QY 721 GAAGCTGAAAAAGTGGGAGCGCCGAGACAGAAACGAGTGGTGAATTTGGCGCTGGA 780
 DB 721 GAAGCTGAAAAAGTGGGAGCGCCGAGACAGAAACGAGTGGTGAATTTGGCGCTGGA 780
 QY 781 GTAACAGCTGAGCCATTTGAATGCTTGAAGTGTGCTGTGCGCGGAGTATCTTCAAC 840
 DB 781 GTAACAGCTGAGCCATTTGAATGCTTGAAGTGTGCTGTGCGCGGAGTATCTTCAAC 840
 QY 841 TTGAAGTGAACGATTTGCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
 DB 841 TTGAAGTGAACGATTTGCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
 QY 901 ATCTCATTTTGGCTGACTGATTTCTCATCTTGAACCTGGAAGAGTGGAAAGCTAGG 960
 DB 901 ATCTCATTTTGGCTGACTGATTTCTCATCTTGAACCTGGAAGAGTGGAAAGCTAGG 960
 QY 961 CCACAAATTTAGGCTCTCTGTGTGATTTAGATTTTACTGCAATTTTTCGCAATTTGCT 1020
 DB 961 CCACAAATTTAGGCTCTCTGTGTGATTTAGATTTTACTGCAATTTTTCGCAATTTGCT 1020
 QY 1021 TTTTGGGCGCAAAACCTTCTGCGGTAATTAATTAATTAATTAATTAATTAATTAATTA 1080
 DB 1021 TTTTGGGCGCAAAACCTTCTGCGGTAATTAATTAATTAATTAATTAATTAATTAATTA 1080
 QY 1081 GTCAAAAACCTTGAACCTTCTGCGGTAATTAATTAATTAATTAATTAATTAATTAATTA 1140
 DB 1081 GTCAAAAACCTTGAACCTTCTGCGGTAATTAATTAATTAATTAATTAATTAATTAATTA 1140
 QY 1141 CATTTTCAAAAGTACCTTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
 DB 1141 CATTTTCAAAAGTACCTTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
 QY 1201 GTGGGCTCTTCCAACTCCCGGCAAAATTCCTGTACGCGTACGAGCTTTGTATTAATTTT 1260
 DB 1201 GTGGGCTCTTCCAACTCCCGGCAAAATTCCTGTACGCGTACGAGCTTTGTATTAATTTT 1260
 QY 1261 TTCAAATTTGTTTCTCTACAAACAAAAAAGGTTCAAAAAA 1315

Db 1261 TTCAAATTTGTTTCTCTCTACAAACAAAAAAGGTTCAAAAAA 1315
 RESULT 14
 US-07-927-681-1
 ? Sequence 1, Application US/07927681
 ? GENERAL INFORMATION:
 ? APPLICANT: Horvitz, H. Robert
 ? APPLICANT: Hengartner, Michael
 ? TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 ? TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL
 ? TITLE OF INVENTION: DEATH AND USES THEREFOR
 ? NUMBER OF SEQUENCES: 5
 ? CORRESPONDENCE ADDRESSES:
 ? ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 ? STREET: Two Millenia Drive
 ? CITY: Lexington
 ? STATE: Massachusetts
 ? COUNTRY: U.S.A.
 ? ZIP: 02173-4799
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/07/927,681
 ? FILING DATE: 10-AUG-1992
 ? CLASSIFICATION: 424
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Granahan, Patricia
 ? REGISTRATION NUMBER: 32,227
 ? REFERENCE/DOCKET NUMBER: MIT-5934A
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (617) 861-6240
 ? TELEFAX: (617) 861-9540
 ? TELEX: 951794
 ? INFORMATION FOR SEQ ID NO: 1:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 6559 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: double
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA (genomic)
 ? US-07-927-681-1
 Query Match 48.1%; Score 632.6; DB 3; Length 6559;
 Best Local Similarity 99.8%; Pred. No. 4.4e-133;
 Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 669 GGAGCACTTTCATGACACTCGGAAACAAATGAAAGAGACTACGAACGAGCAAGAGCTGA 728
 DB 3392 GGAGCACTTTCATGACACTCGGAAACAAATGAAAGAGAGCTACGAACGAGCAAGAGCTGA 3451
 QY 729 AAAAGTGGGAGCGCCGGAAGACAGACGCTGCTGATGATTGGCGCTGGAGTAACAGC 788
 DB 3452 AAAAGTGGGAGCGCCGGAAGACAGACGCTGCTGATGATTGGCGCTGGAGTAACAGC 3511
 QY 789 TGGAGCATTGGAATGCTTGGAGTCTGCTGTGTGGCGGATGATGTTCAAGCTTGAAGTA 848
 DB 3512 TGGAGCATTGGAATGCTTGGAGTCTGCTGTGTGGCGGATGATGTTCAAGCTTGAAGTA 3571
 QY 849 ACGTATTCATTTGTGTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
 DB 3572 ACGTATTCATTTGTGTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3631
 QY 909 TTGCTACTGATTTCTCTACTCTTTGAAGTGAAGAGGGAAGGCTAGGCAACAAT 968
 DB 3632 TTGCTACTGATTTCTCTACTCTTTGAAGTGAAGAGGGAAGGCTAGGCAACAAT 3691
 QY 969 TAGGCTCTGCTGTGATTTAGATTTTCTCAATTTTTCGATTTGCTTTT 1028

Db 3692 TAGGCTCTCTGTGATGATTTACGATTTTACTGCAATTTTTCGATTTGCTTTT 3751
 QY 1029 GGCCAAACCTACTTCCGCGTAATATCACTTTCCGTGTTGTGATTTGCTCAAAA 1088
 Db 3752 GGCCAAACCTACTTCCGCGTAATATCACTTTCCGTGTTGTGATTTGCTCAAAA 1088
 QY 1089 CCCTGAAACCTACTTTTTCGCGGTAGCCCTGCGCTTCTCTGCAATTTGCA 1148
 Db 3812 CCCTGAAACCTACTTTTTCGCGGTAGCCCTGCGCTTCTCTGCAATTTGCA 1148
 QY 1149 AAGTACCCCTGATCTCAATATTCATCTTCACTTTACTGTCCTTTGATGCTTC 1208
 Db 3872 AAGTACCCCTGATCTCAATATTCATCTTCACTTTACTGTCCTTTGATGCTTC 1208
 QY 1209 TTCCAACTCCCGCAATTCCTGACGCGTACGCGACTTGTATTTATTTTCAATT 1268
 Db 3932 TTCCAACTCCCGCAATTCCTGACGCGTACGCGACTTGTATTTATTTTCAAAAT 1268
 QY 1269 GTTTTCTCTCTACACAAACAAAAAGGCTTC 1301
 Db 3992 GTTTTCTCTCTACACAAACAAAAAGGCTTC 4024

RESULT 15

US-08-288-295-1
 : Sequence 1, Application US/08288295
 : GENERAL INFORMATION:
 : APPLICANT: Horvitz, H. Robert
 : APPLICANT: Hengartner, Michael
 : TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 : TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Fish & RICHARDSON
 : STREET: 225 Franklin Street, Suite 3100
 : CITY: Boston
 : STATE: Massachusetts
 : COUNTRY: U.S.A. (F) ZIP: 02110-2804
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: WordPerfect 5.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/288,295
 : FILING DATE: 10-AUG-1994
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/927,681
 : FILING DATE: 10-AUG-1992
 : CLASSIFICATION: 514
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Clark, Paul T.
 : REGISTRATION NUMBER: 30,162
 : REFERENCE/DOCKET NUMBER: 01997/201003
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (617) 542-5070
 : TELEFAX: (617) 542-8906
 : TELEX: 200154
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 6559 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : US-08-288-295-1

Query Match 48.1%; Score 632.6; DB 6; Length 6559;
 Best Local Similarity 99.8%; Pred. No. 4.4e-133;
 Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 669 GGAGGACTTCTGACACTCGGAAACAAATGAAGAGGACTAGACAGAGCAAGCTGA 728
 Db 3392 GGAGGACTTCTGACACTCGGAAACAAATGAAGAGGACTAGACAGAGCAAGCTGA 728
 QY 729 AAAAGTGGAGCGCCGGAAGAGCAAGAGAGGAGGATGAGGCTGAGAGTAAACAG 788
 Db 3452 AAAAGTGGAGCGCCGGAAGAGCAAGAGAGGAGGATGAGGCTGAGAGTAAACAG 788
 QY 789 TGGAGCCATTGGAATCGTTGAGAGTGTGTGTGGCGGATGATGTTGAGTTGAAGTA 848
 Db 3512 TGGAGCCATTGGAATCGTTGAGAGTGTGTGTGGCGGATGATGTTGAGTTGAAGTA 848
 QY 849 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
 Db 3572 ACGTATTCATTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 908
 QY 909 TTTGCTCTCTGATTTCTCTATCTTGAACGTGGAAGAGTGGAAAGCTAGGCCAAT 968
 Db 3632 TTTGCTCTCTGATTTCTCTATCTTGAACGTGGAAGAGTGGAAAGCTAGGCCAAT 968
 QY 969 TAGGCTCTCTGTGATTTTACGATTTTACGATTTTTCGATTTGCTTTT 1028
 Db 3692 TAGGCTCTCTGTGATTTTACGATTTTACGATTTTTCGATTTGCTTTT 1028
 QY 1029 GGCCAAACCTACTTCCGCGTAATATCAACTTTCCGTGTAATTTTCGATTTGCTTTT 3751
 Db 3752 GGCCAAACCTACTTCCGCGTAATATCAACTTTCCGTGTAATTTTCGATTTGCTTTT 3751
 QY 1089 CCCTGAAACCTACTTTTTCGCGGTAGCCCTGCGCTTCTCTGCAATTTGCA 1148
 Db 3812 CCCTGAAACCTACTTTTTCGCGGTAGCCCTGCGCTTCTCTGCAATTTGCA 1148
 QY 1149 AAGTACCCCTGATCTCAATATTCATCTTCACTTTACTGTCCTTTGATGCTTC 1208
 Db 3872 AAGTACCCCTGATCTCAATATTCATCTTCACTTTACTGTCCTTTGATGCTTC 1208
 QY 1209 TTCCAACTCCCGCAATTCCTGACGCGTACGCGACTTGTATTTATTTTCAAAAT 1268
 Db 3932 TTCCAACTCCCGCAATTCCTGACGCGTACGCGACTTGTATTTATTTTCAAAAT 1268
 QY 1269 GTTTTCTCTCTACACAAACAAAAAGGCTTC 1301
 Db 3992 GTTTTCTCTCTACACAAACAAAAAGGCTTC 4024

Search completed: February 28, 2003, 08:43:11
 Job time : 2512.41 secs

GenCore version 5.1.4.P5_4578
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 20:35:45 : Search time 620.847 Seconds
(without alignments)
3609.239 Million cell updates/sec

Title: US-09-993-420a-2

Perfect score: 1315
Sequence: 1 ttgagatgacacgcctgcac.....cggttcaaaaaaaaaaaaaa 1315

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3936061 seqs, 852009584 residues

Total number of hits satisfying chosen parameters: 7872122

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents, NA, New: *
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2: /cgn2_6/prodata/2/pna/US07_NEW_COMB.seq:*
3: /cgn2_6/prodata/2/pna/US08_NEW_COMB.seq:*
4: /cgn2_6/prodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/prodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/prodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40.4	3.1	4620	US-10-144-771-6694	Sequence 6694, Ap
2	39.6	3.0	364	US-09-531-113-3558	Sequence 3558, Ap
3	38.4	2.9	8323	US-10-311-455-31	Sequence 31, Appl
4	38.2	2.9	6322	US-10-310-673-2117	Sequence 665, App
5	38	2.9	369	US-10-310-673-2117	Sequence 2117, Ap
6	38	2.9	502	US-09-531-113-6153	Sequence 6153, Ap
7	38	2.9	17848	US-10-240-453-37	Sequence 37, Appl
8	38	2.9	17848	US-10-257-166-57	Sequence 57, Appl
9	37.8	2.9	417	US-09-513-999C-28718	Sequence 28718, A
10	37.4	2.8	6229	US-10-311-455-237	Sequence 237, App
11	37.2	2.8	297	US-10-310-673-1846	Sequence 1846, Ap
12	37.2	2.8	15732	US-10-240-453-108	Sequence 108, Appl
13	37	2.8	180216	US-10-308-485-6	Sequence 6, Appl
14	36.8	2.8	425	US-09-531-113-12891	Sequence 12891, A
15	36.8	2.8	5317	US-10-311-455-581	Sequence 581, App
16	36.6	2.8	1825	US-60-427-313-7	Sequence 2359, Ap
17	36.6	2.8	1840	US-10-017-161-2359	Sequence 1648, Ap
18	36.6	2.8	9206	US-10-311-455-1648	Sequence 71, Appl
19	36.6	2.8	9964	US-10-311-455-71	Sequence 3971, Appl
20	36.4	2.8	414	US-09-531-113-3971	Sequence 30591, A
21	36.4	2.8	431	US-09-724-676-30591	Sequence 30591, A
22	36.4	2.8	478	US-09-724-676-30585	Sequence 30585, A
23	36.4	2.8	478	US-09-724-676-30585	Sequence 30585, A
24	36.4	2.8	523	US-09-724-676-30588	Sequence 30588, A
25	36.4	2.8	523	US-09-724-676-30588	Sequence 30588, A
26	36.4	2.8	523	US-09-724-676-30588	Sequence 30588, A

C 27	36.4	2.8	570	US-09-724-676-30583	Sequence 30583, A
C 28	36.4	2.8	570	US-09-724-676-30583	Sequence 30583, A
C 29	36.4	2.8	634	US-09-724-676-30587	Sequence 30587, A
C 30	36.4	2.8	634	US-09-724-676-30587	Sequence 30587, A
C 31	36.4	2.8	681	US-09-724-676-30582	Sequence 30582, A
C 32	36.4	2.8	681	US-09-724-676-30582	Sequence 30582, A
C 33	36.4	2.8	681	US-09-724-676-30582	Sequence 30582, A
C 34	36.4	2.8	681	US-09-724-676-30582	Sequence 30582, A
C 35	36.4	2.8	728	US-09-724-676-30581	Sequence 30581, A
C 36	36.4	2.8	728	US-09-724-676-30581	Sequence 30581, A
C 37	36.4	2.8	891	US-09-724-676-30590	Sequence 30590, A
C 38	36.4	2.8	891	US-09-724-676-30590	Sequence 30590, A
C 39	36.4	2.8	959	US-09-724-676-30579	Sequence 30579, A
C 40	36.4	2.8	959	US-09-724-676-30579	Sequence 30579, A
C 41	36.4	2.8	983	US-09-724-676-30598	Sequence 30598, A
C 42	36.4	2.8	983	US-09-724-676-30597	Sequence 30597, A
C 43	36.4	2.8	1094	US-09-724-676-30597	Sequence 30597, A
C 44	36.4	2.8	1094	US-09-724-676-30596	Sequence 30596, A
C 45	36.4	2.8	1132	US-09-724-676-30596	Sequence 30596, A

ALIGNMENTS

RESULT 1
US-10-144-771-6694
Sequence 6694, Application US/10144771
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
FILE REFERENCE: C1001321
CURRENT APPLICATION NUMBER: US/10/144,771
CURRENT FILING DATE: 2002-05-15
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 6694
LENGTH: 4620
TYPE: DNA
ORGANISM: HUMAN
US-10-144-771-6694

Query Match
Best Local Similarity 48.7%; Pred. No. 1.1;
Matches 110; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1055 CAACCTTCCGCTGCTCTGATATTCGCAAAACCCGAAACCCCTACTTTCGCG 1114
DB 2983 CAACATACCCCCCAATAGTATTTCTTCCCTGCTGCTCCCTCCCTCCAT 3042
QY 1115 TGGCTACGCTCCGCTCTCTCCACATTTCCAAAGACCCGATTCATATTC 1174
DB 3043 TTCCGCCCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3102
QY 1175 TCTTCACCTTACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3124
DB 3103 CTGCT 3162
QY 1235 GCGTACGCACTTGTATTTATTTTTCAAATGTTTCTCTA 1280
DB 3163 CTGCTA 3208

RESULT 2
US-09-531-113-3558/c
Sequence 3558, Application US/09531113
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(15761)B
CURRENT APPLICATION NUMBER: US/09/531, 113
CURRENT FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 48629
SEQ ID NO 3558
LENGTH: 364
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: jC-gmfl02220056g02a1
US-09-531-113-3558

Query Match 3.0%; Score 39.6; DB 5; Length 364;
Best Local Similarity 72.9%; Pred. No. 0.8; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 19;

QY 1246 TTGTATATATTTTCTCAATGTTTCTCTACACACAAAAACGGTTCAAA 1305
DB 1332 TTTTATTTTATTTTCTCCCTTTTCTTTTTCACAAAAAATTTTAAAAA 73

QY 1306 AAAAAAAA 1315
DB 72 AAAAAAAA 63

RESULT 3
US-10-311-455-31/C
Sequence 31, Application US/10311455

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPERBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311.455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 31
LENGTH: 8323
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-31

Query Match 2.9%; Score 38.4; DB 6; Length 8323;
Best Local Similarity 51.1%; Pred. No. 4.7;
Matches 90; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 1140 ACATTTCAAGTACCCCTGATTCATATTCATCTTCACTTAAGTCTCTTTCG 1199
DB 4792 AATTTAAATATTAATTAATTAATTTCTCTCTCTCTCTCTCTCTCTCTCA 4733
QY 1200 TGTGGCTCTTCACTCCCAATTCCTGACGCGTACGCGACTTTGATTTATTT 1259
DB 4733 AATTTCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4673
QY 1260 TTTCAATTTGTTCTCTCTACACACAAAAACGGTTCAAAAA 1315
DB 4672 AATCAATTAATCACTCACTTAATTAATCAAAAGATACAAATTAATTAATTA 4617

RESULT 4
US-10-311-455-665/C
Sequence 665, Application US/10311455

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPERBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation

TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311.455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 665
LENGTH: 6222
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-665

Query Match 2.9%; Score 38.2; DB 6; Length 6222;
Best Local Similarity 52.1%; Pred. No. 4.9; Indels 78; Gaps 0;
Matches 85; Conservative 0; Mismatches 78;

QY 1153 ACCCTGATATCATTAATTCATCTTCACTTAAGTCTCTTTCGTTGGCTTCC 1212
DB 5449 AACGCTATTAATTTTAAATAAACCTTTCATCTTCTTATTAATTAATTTTCC 5390
QY 1213 AACTCCCCCAATTCCTGACGCGTACGCGACTTTGATTTATTTTCAATGTT 1272
DB 5389 AATCTCTTAATTAATTAATTTCAATCTAAATAATTAATTAATTAATTTCTT 5330
QY 1273 TCTCTACACACAAAAAAGCGTCAAAAAA 1315
DB 5329 ACTATTAACACAAAAAATCATTTTCAATTAATAAAAAA 5287

RESULT 5
US-10-310-673-2117
Sequence 2117, Application US/10310673

GENERAL INFORMATION:
APPLICANT: Garcia, Pablo
APPLICANT: Escobedo, Jaime
APPLICANT: Lamson, George
APPLICANT: Randazzo, Filippo
APPLICANT: Molter, Edward
APPLICANT: Klingner, Ullie
APPLICANT: Janatpour, Mary Jo
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS PROSTATE CELLS AND THEIR METHODS OF USE
FILE REFERENCE: 18095.002
CURRENT APPLICATION NUMBER: US/10/310.673
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/336,613
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 2164
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2117
LENGTH: 369
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-673-2117

Query Match 2.9%; Score 38; DB 6; Length 369;
Best Local Similarity 51.1%; Pred. No. 2.2;
Matches 89; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1132 TCTCTCCACATTTCCAAAGTACCCCTGATTCATATTCATCTTCACTTAAGTTC 1191
DB 63 TCTTTTATTAATTCCTTTTAAATAATTCAGCTCAATTCACACCACTCAACTCTC 122
QY 1192 TCTTTGCTGCGCTCTTCCACTCCCAATTCCTTACGCGGACGACTTTGTA 1251
DB 123 TCTTTCCAGCTACTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 182

14312 AAACCTCCTCTTAATACCAAAACACCCCTATCT-ACAAAAAACCATCTTCTTCAACCA 14254

```
QY 1189 GTCCTTTTCTGTCGCTCTTCACACGCCCCCAAAATTCGTACGGGTACGCGACTTT 1248
; SEQ ID NO 237
; LENGTH: 6229
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-237
Db 14193 CTAATCTTCTCTTAAATAAATAATCTCTATCACCACCAACTAAATACAAATATAT 14134
QY 1249 GATATTTATTTTTCATATGTTTCTCTCTACACACACAAAAAAGCGTTCAAAAAA 1308
; SEQ ID NO 1310
; LENGTH: 14132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: v=a or c or g
US-09-513-999C-28718/c
; Sequence 28718, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 28718
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 348
; OTHER INFORMATION: v=a or c or g
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: w=a or t
US-09-513-999C-28718
Query Match 2.9%; Score 37.8; DB 5; Length 417;
Best Local Similarity 60.0%; Pred. No. 2.6;
Matches 63; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 669 GAGCAGCTTCATGACACTCGGAAAAAATGAAAGAGACTACGACGACGAGAGCTGA 728
; SEQ ID NO 108
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: w=a or t
US-09-513-999C-28718
Db 108 GGAATATTTCTTGACACTAGAGATGCAATGAAAGACTGTGGAGATATGAGAGCTCC 49
QY 729 AAAAGTGGAGCGCGGAGAGACAGACAGCGGTGTCATGATGG 773
; SEQ ID NO 48
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: w=a or t
US-09-513-999C-28718
Db 48 TGAAGTGGAGCGCGGAGAGACAGACAGCGGTGTCATGATGG 4
RESULT 10
US-10-311-455-237/c
; Sequence 237, Application US/10311455
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 237
; LENGTH: 6229
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-237
Query Match 2.8%; Score 37.4; DB 6; Length 6229;
Best Local Similarity 58.6%; Pred. No. 8.1;
Matches 65; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 1205 CCTCTCCACTCCGCCCAATTCCTGACGCGGACGACTTGAATTTATTTTCA 1264
; SEQ ID NO 1162
; LENGTH: 1162
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-237
Db 1162 CCTAAACGACACATCTATCTTCTCTCAATTAACATATTTATTTATTTAT 1103
QY 1265 AATTGTTTCTCTCTACACACAAAAAAGCGTTCAAAAA 1315
; SEQ ID NO 1102
; LENGTH: 1102
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-237
Db 1102 TTTCTAAATTTTACCAAAAAA 1052
RESULT 11
US-10-310-673-1846
; Sequence 1846, Application US/10310673
; GENERAL INFORMATION:
; APPLICANT: Garcia, Pablo
; APPLICANT: Escobedo, Jaime
; APPLICANT: Lamsom, George
; APPLICANT: Randazzo, Filippo
; APPLICANT: Molier, Edward
; APPLICANT: Klinger, Julie
; APPLICANT: Jaatpour, Mary Jo
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE REFERENCE: 18095.002
; CURRENT APPLICATION NUMBER: US/10/310,673
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/336,613
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1846
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-673-1846
Query Match 2.8%; Score 37.2; DB 6; Length 297;
Best Local Similarity 55.4%; Pred. No. 3.3;
Matches 72; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 1132 TCTCTCCACTTCCTCAAGTACCCCTGTATCTCAATTAATTCATCTTCACTT 1191
; SEQ ID NO 66
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-237
Db 66 TCTGTACTATCTATCTTAAATAATTCAGTCAATTCATCAACCACTCCAACTCC 125
QY 1192 TCTTTCTGTCGCTCTTCACACGCCCCCAAAATTCGTACGGGTACGCGACTTT 1251
; SEQ ID NO 126
; LENGTH: 126
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-237
Db 126 TCTTTCTGTCGCTCTTCACACGCCCCCAAAATTCGTACGGGTACGCGACTTT 1251
QY 1252 TTTATTTT 1261
; SEQ ID NO 186
; LENGTH: 186
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-237
Db 186 TTTATTTT 195
RESULT 12
US-10-240-453-108/c
; Sequence 108, Application US/10240453
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
```

```
; TITLE OF INVENTION: Transcription
; TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
; FILE REFERENCE: 5013.1009
; CURRENT APPLICATION NUMBER: US/10/240,453
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03973
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 108
; LENGTH: 15732
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-240-453-108
```

```
Query Match
Best Local Similarity 47.1%; Score 37.2; DB 6; Length 15732;
Matches 114; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
```

```
QY 867 AATAATTATTTATGACACCTCTTACATTTGATTCATTTTGGCTGATTTCTCT 926
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8134 AATAATTCCTTTTACGATCTCCACCAACACTAATTTCTAATAATTTATTTT 8075
QY 927 CATCCTTGAACGAGAGTGGAAGCTAGCCACAAATTCAGGCTCTGTGCGA 986
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8074 AACCAATACCAAAACATCATCTTAACACGCGATTTATATCATATATTTTAA 8015
QY 987 TTACGATTTTCGCAATTTTTCGCCATTTTTCGCTTTTTCGCTTTCGCTTTCG 1046
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8014 TATTTATCTCTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 7955
QY 1047 CGTAATATCACTTTCCGCTGTCGTACATTTGCTCAAAAACCCCAACCCCACT 1106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 7954 TTAACATACATCATATATATCTTATTAACCATTTATATACACCTTTAAAAA 7895
QY 1107 TC 1108
    ||
DB 7894 TC 7893
```

```
RESULT 13
US-10-308-485-6
; Sequence 6, Application US/10308485
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/10/308,485
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/835,232
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 180216
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)...(180216)
; OTHER INFORMATION: n = A,T,C or G
US-10-308-485-6
```

```
Query Match
Best Local Similarity 57.3%; Score 37; DB 6; Length 180216;
Matches 67; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
```

```
QY 664 AGCTGGGACGACCTTCATGACACTCGGAAAAATGAAAGAGACTACGACGACGAA 723
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 19646 AGCTGGGACGACGAGAGTACGACCTCCAAACAAACAAACAAACAAACAAAC 19705
QY 724 GCTGAAAAAAGTGGGACCGCGAAGACAGACAGCGGTGCGATGATTGGCGCTGA 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 19706 AAAACACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 19762
```

```
RESULT 14
US-09-531-113-12891
; Sequence 12891, Application US/09531113
; GENERAL INFORMATION:
```

```
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15761)B
; CURRENT APPLICATION NUMBER: US/09/531,113
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 48629
; SEQ ID NO 12891
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: jc-gmfl02220143a08d1
US-09-531-113-12891
```

```
Query Match
Best Local Similarity 69.4%; Score 36.8; DB 5; Length 425;
Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
```

```
QY 1244 ACTTGATATATTTTTCATATTTGTTCTCTCTACACACAAACAAACGTTCAA 1303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 72 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATA 131
QY 1304 AAAAAAAAAA 1315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 AAAAAAAAAA 143
```

```
RESULT 15
US-10-311-455-581/C
; Sequence 581, Application US/10311455
; GENERAL INFORMATION:
; APPLICANT: Olek, Alexander
; APPLICANT: Piepenbrock, Christian
; APPLICANT: Berlin, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 581
; LENGTH: 5317
; TYPE: DNA
; ORGANISM: Artificial Sequence
```


FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-581

Query Match 2.8%; Score 36.8; DB 6; Length 5317;
Best Local Similarity 49.5%; Pred. No. 11;

Matches 95; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

```
OY 1123 CCTCCGCTCTCTCCACATTTCCAAAGTACCCCTGATCTCAATATATCTTCACT 1182
    || || || || || || || || || || || || || || || || || || || ||
DB 4812 CCACCCACGCTCTCTATCTAACCACCTCCCGCCGATTTCTAATCAACACAAAT 4753
    || || || || || || || || || || || || || || || || || || || ||
OY 1183 TTAAGTGTCTTTGCTGCGCTCTTCCAACTCCCGCCAAATCTGTAGCGGTACGC 1242
    || || || || || || || || || || || || || || || || || || || ||
DB 4752 TTATATTTTATTTTATTTTCAACCCCTAACCTTAATCCAACTCTTAAACCTTATTC 4693
    || || || || || || || || || || || || || || || || || || || ||
OY 1243 GACTTGTATTTATTTTTCAAATTTGTTTCTCTCTACACACAAAAAAGGTTCA 1302
    || || || || || || || || || || || || || || || || || || || ||
DB 4692 TTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTATCG 4633
    || || || || || || || || || || || || || || || || || || || ||
OY 1303 AAAAAAAAAA 1314
    || || || || || || || || || || || || || || || || || || || ||
DB 4632 CCCAAACTAAAA 4621
    || || || || || || || || || || || || || || || || || || || ||
```

Search completed: February 28, 2003, 17:23:11
Job time : 708.847 secs

GenCore version 5.1.4.P5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 27, 2003, 18:42:50 ; Search time 1592.53 Seconds

(without alignments)
13373.121 Million cell updates/sec

Title: US-09-993-420A-2

Perfect score: 1315

Sequence: 1 ttgagatgacacgctgcac.....cgttcaaaaaaaaaaaaaaa 1315

Scoring table:

IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_estl3:*
13: gb_estl4:*
14: gb_estl5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	372	28.3	372	9	AV186746
2	360	27.4	360	14	AV186746
3	355	27.0	375	14	C39347
4	314.6	23.9	323	14	C42506
5	299	22.7	300	9	D73048
6	295.6	22.5	360	9	AV181369
					AV191206

C 7	279.6	21.3	300	14	C39078	C39078	C39078	Yuj1
C 8	275.6	21.0	300	14	C31912	C31912	C31912	Yuj1
C 9	269.2	20.5	300	14	C29364	C29364	C29364	Yuj1
C 10	261	19.8	360	9	AV193616	AV193616	AV193616	Yuj1
C 11	259.4	19.7	300	9	AV179317	AV179317	AV179317	Yuj1
C 12	68.4	5.2	1101	17	CNS0106X	AL098595	Drosophila	
C 13	68.4	5.0	1101	17	CNS0039G	AL065921	Drosophila	
C 14	65.2	5.0	997	17	CNS005TE	AL060767	Drosophila	
C 15	56.6	4.3	1101	17	CNS0182P	AL108811	Drosophila	
C 16	53.2	4.0	1101	17	CNS0039G	AL066537	Drosophila	
C 17	52.4	4.0	1101	17	CNS0039G	AL108772	Drosophila	
C 18	50.4	3.8	987	17	CNS00418	AL066537	Drosophila	
C 19	49.6	3.8	1201	17	CNS016DO	AL075264	Drosophila	
C 20	49.6	3.7	1201	17	CNS00418	AL075264	Drosophila	
C 21	48.8	3.7	1201	17	CNS016DO	AL075264	Drosophila	
C 22	48.6	3.7	808	10	BE033818	BE033818	ME6H07 M	
C 23	48	3.7	1201	17	CNS016DO	AL075264	Drosophila	
C 24	47.8	3.6	925	17	CNS00DSE	AG045123	Pan trogl	
C 25	47.6	3.6	801	17	AG045123	BE966968	60160935	
C 26	47.6	3.6	850	12	BE966968	AL514493	AL514493	
C 27	47.4	3.6	762	9	AL514493	AL106382	Drosophila	
C 28	47.2	3.6	908	17	CNS016DO	AL106382	Drosophila	
C 29	47.2	3.6	1204	17	CNS016DO	AL106382	Drosophila	
C 30	45.8	3.5	411	9	AL1635287	AL1635287	tz80c06 x	
C 31	45.8	3.5	914	17	BH152037	BH152037	ENTP104NF	
C 32	45.8	3.5	935	17	CNS010G4	AL098926	Drosophila	
C 33	45.8	3.5	1183	17	CNS016CR	AL106511	Drosophila	
C 34	45.2	3.4	1201	17	CNS016CR	AL106511	Drosophila	
C 35	45	3.4	421	10	AM460090	AM460090	si10a12.y	
C 36	45	3.4	583	9	CNS044OG	AL274417	Tetraodon	
C 37	45	3.4	633	9	AL513979	AL513979	AL513979	
C 38	44.8	3.4	394	9	AL1491775	AL1491775	ts94h05 x	
C 39	44.8	3.4	920	17	AZ691914	AZ691914	ENTM267R	
C 40	44.8	3.4	1101	17	CNS016RG	AL107110	Drosophila	
C 41	44.6	3.4	450	9	AL513867	AL513867	AL513867	
C 42	44.6	3.4	527	9	AL514325	AL514325	AL514325	
C 43	44.6	3.4	1179	17	CNS001CW	AL060645	Drosophila	
C 44	44.4	3.4	882	17	CNS00CEK	AL058777	Drosophila	
C 45	44.2	3.4	504	14	B0524016	B0524016	NISC_no02	

ALIGNMENTS

RESULT 1
AV186746
LOCUS
DEFINITION
AV186746 yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans CDNA clone yk503f3 5', mRNA sequence.
ACCESSION
AV186746
VERSION
AV186746.1 GI:5568729
KEYWORDS
EST.
ORGANISM
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Pelodieridae; Caenorhabditis.
REFERENCE
1 (bases 1 to 372)
Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsui, H.,
Nishigaki, A., Morinashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano
, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and
Nomoto, H.

Expressed genes in C.elegans
Unpublished (1999)
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1..372
/organism="Caenorhabditis elegans"

FEATURES
source

```

/strain="N2"
/db_xref="taxon:6239"
/clone="yk503f3"
/clone_lib="Yui Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT      105 a      75 c      118 g      74 t
ORIGIN

```

```

Query Match      28.3%; Score 372; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 5.2e-68;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 2 TTGAGATGACAGCGTCGACGCGGACGACGTCGTCGACGATCCGCGTATCGGCGAGAA 61
    |||||||
DB 1 TTGAGATGACAGCGTCGACGCGGACGACGTCGTCGACGATCCGCGTATCGGCGAGAA 60
    |||||||
OY 62 CGATGGCGACTGGCGAGATGAAGAGTTCTGCGGATTAAGGACACAGAGCCCGAGATT 121
    |||||||
DB 61 CGATGGCGACTGGCGAGATGAAGAGTTCTGCGGATTAAGGACACAGAGCCCGAGATT 120
    |||||||
OY 122 TTGGAATCAATAGTGAATGCTGAGGACTTGCATACCGAGTAGAGCGCTTGCAGCGGAA 181
    |||||||
DB 121 TTGGAATCAATAGTGAATGCTGAGGACTTGCATACCGAGTAGAGCGCTTGCAGCGGAA 180
    |||||||
OY 182 GAATGTCATCGAGAGATCAATTGATGAAAAATCAATGATGGAGAGCCAGAGCTTG 241
    |||||||
DB 181 GAATGTCATCGAGAGATCAATTGATGAAAAATCAATGATGGAGAGCCAGAGCTTG 240
    |||||||
OY 242 ATATCGAGGATTTGTGTCGATATTTCCGACCGGAATCCGGCAAAAGCAATGGAAT 301
    |||||||
DB 241 ATATCGAGGATTTGTGTCGATATTTCCGACCGGAATCCGGCAAAAGCAATGGAAT 300
    |||||||
OY 302 GATTGGAGACCGGAGATTCCGTCGTGAGTGCACCGGAGCAGCAATGATGCGAGTTA 361
    |||||||
DB 301 GATTGGAGACCGGAGATTCCGTCGTGAGTGCACCGGAGCAGCAATGATGCGAGTTA 360
    |||||||
OY 362 TGGGACGATAT 373
    |||||||
DB 361 TGGGACGATAT 372
    |||||||

```

```

RESULT 2
C39347      360 bp      mRNA      linear      EST 18-OCT-1999
LOCUS      C39347 Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo
DEFINITION Caenorhabditis elegans cDNA clone yk201b10 5', mRNA sequence.
ACCESSION  C39347
VERSION     C39347.1 GI:2375584
KEYWORDS   EST.
SOURCE      Caenorhabditis elegans.
ORGANISM   Caenorhabditis elegans.
REFERENCE  1 (bases 1 to 360)
AUTHORS    Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
            'M., Miyata,A. and Nishigaki,A.
TITLE      Expression map of the C.elegans genome
JOURNAL    Unpublished (1996)
COMMENT    Contact: Yui Kohara
            National Institute of Genetics
            Genome Biology Lab.
            Yata 1111, Mishima, Shizuoka 411, Japan
            Tel: 81-559-81-6854
            Fax: 81-559-81-6855
            Email: ykohara@lab.nig.ac.jp.
FEATURES   location/Qualifiers
            1..360
            /organism="Caenorhabditis elegans"
            /strain="N2"
            /db_xref="taxon:6239"
            /clone="yk201b10"

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/clone_lib="Yui Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT      106 a      69 c      114 g      71 t
ORIGIN

```

```

Query Match      27.4%; Score 360; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.7e-65;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 38 CGATCCGCGGCTATCGCGGACGAGATGCGGCTGCGGATGAAGGAGCTTCTGCGGGA 97
    |||||||
DB 1 CGATCCGCGGCTATCGCGGACGAGATGCGGCTGCGGATGAAGGAGCTTCTGCGGGA 60
    |||||||
OY 98 TAAAGGACAGAGCCCGACGATTTTGAATCAATAGTATGCTCAGAGCTTGCATCAC 157
    |||||||
DB 61 TAAAGGACAGAGCCCGACGATTTTGAATCAATAGTATGCTCAGAGCTTGCATCAC 120
    |||||||
OY 158 CGACTAGGCAAGCTTTCAGCGGAGAAATGTCATCGAGATCAATTGATGAAAAATCA 217
    |||||||
DB 121 CGACTAGGCAAGCTTTCAGCGGAGAAATGTCATCGAGATCAATTGATGAAAAATCA 180
    |||||||
OY 218 ATGATGGGAAAGACCAAGCTTATATGAGAGGATTTGTGTCGATATTTCCAGCACC 277
    |||||||
DB 181 ATGATGGGAAAGACCAAGCTTATATGAGAGGATTTGTGTCGATATTTCCAGCACC 240
    |||||||
OY 278 GAATCCGCGCAAGGAAATGATGTTTGGAGCAGCGGATTTGCCGTGAGTGCAC 337
    |||||||
DB 241 GAATCCGCGCAAGGAAATGATGTTTGGAGCAGCGGATTTGCCGTGAGTGCAC 300
    |||||||
OY 338 CGGACGACGAATGATGCGGATTTATGGAACGATATTCGAAAGACAGCGGAAATT 397
    |||||||
DB 301 CGGACGACGAATGATGCGGATTTATGGAACGATATTCGAAAGACAGCGGAAATT 360
    |||||||

```

```

RESULT 3
C42506      375 bp      mRNA      linear      EST 18-OCT-1999
LOCUS      C42506 Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo
DEFINITION Caenorhabditis elegans cDNA clone yk312c5 5', mRNA sequence.
ACCESSION  C42506
VERSION     C42506.1 GI:2378743
KEYWORDS   EST.
SOURCE      Caenorhabditis elegans.
ORGANISM   Caenorhabditis elegans.
REFERENCE  1 (bases 1 to 375)
AUTHORS    Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
            'M., Miyata,A. and Nishigaki,A.
TITLE      Expression map of the C.elegans genome
JOURNAL    Unpublished (1996)
COMMENT    Contact: Yui Kohara
            National Institute of Genetics
            Genome Biology Lab.
            Yata 1111, Mishima, Shizuoka 411, Japan
            Tel: 81-559-81-6854
            Fax: 81-559-81-6855
            Email: ykohara@lab.nig.ac.jp.
FEATURES   location/Qualifiers
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            /organism="Caenorhabditis elegans"
            /strain="N2"
            /db_xref="taxon:6239"
            /clone="yk312c5"
            /clone_lib="Yui Kohara unpublished cDNA:Strain N2
            hermaphrodite embryo"
            /sex="hermaphrodite"
            /dev_stage="embryo"

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```

BASE COUNT      107 a      77 c      118 g      72 t      1 others
ORIGIN

```

Query Match 27.0%; Score 355; DB 14; Length 375;
 Best Local Similarity 99.7%; Pred. No. 1,9e-64;
 Matches 366; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 10 ACAGCTTCACGGGGGACACTGCTGACGAATCCGGGATTCGGGACGACGAACGATGGCG 69
 |||||||
 Db 1 ACAGCTTCACGGGGGACACTGCTGACGAATCCGGGATTCGGGACGACGAACGATGGCG 60

QY 70 ACTGGCGAGATGAAGGAGTTTCT-GGGGATTAAGGACAGAGAGCCGCCGATTTTGAAT 128
 |||||||
 Db 61 ACTGGCGAGATGAAGGAGTTTCTGGGGATTAAGGACAGAGAGCCGCCGATTTTGAAT 120

QY 129 CAATAGTGAATGCTCAGGACTTGGCATTGACGAGTAGGACAGCTTCCAGCGGGAAGATGTC 188
 |||||||
 Db 121 CAATAGTGAATGCTCAGGACTTGGCATTGACGAGTAGGACAGCTTCCAGCGGGAAGATGTC 180

QY 189 CATGGAGAGTCAATTTATGAAAAATCATGATTTGGGAAGAGCCGATTTGATATCGA 248
 |||||||
 Db 181 CATGGAGAGTCAATTTATGAAAAATCATGATTTGGGAAGAGCCGATTTGATATCGA 240

QY 249 GGGATTTGTGCTGACTATTTTCACGACGCAATCCGGCAAAAGGAATGGAATGTTTG 308
 |||||||
 Db 241 GGGATTTGTGCTGACTATTTTCACGACGCAATCCGGCAAAAGGAATGGAATGTTTG 300

QY 309 AGACCGGGATTTGCCGTGTGAGTGAACCGGACGACGAATGATGCGATTATGGGAC 368
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 Db 301 AGACCGGGATTTGCCGTGTGAGTGAACCGGACGACGAATGATGCGATTATGGGAC 360

QY 369 GATATTC 375
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 Db 361 GATATTC 367

RESULT 4
 D73048/c 323 bp mRNA linear EST 18-OCT-1999
 LOCUS CELK113B7R Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
 DEFINITION embryo Caenorhabditis elegans cDNA clone yk113b7 3', mRNA sequence.
 ACCESSION D73048
 VERSION D73048.1 GI:1112756
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Pelodierinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 323)
 AUTHORS Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
 Tabara,H.
 TITLE Toward an expression map of the C.elegans genome
 JOURNAL Unpublished (1994)
 COMMENT Contact: Yuji Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: yk@haraelab.nig.ac.jp.
 FEATURES
 source location/Qualifiers
 1..323
 /organism="Caenorhabditis elegans"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone="yk113b7"
 /clone_lib="Yuji Kohara unpublished cDNA:Strain N2
 hermaphrodite embryo"
 /sex="hermaphrodite"
 /dev_stage="embryo"

BASE COUNT 118 a 40 c 96 g 67 t 2 others
 ORIGIN

Query Match 23.9%; Score 314.6; DB 14; Length 323;
 Best Local Similarity 98.1%; Pred. No. 6.1e-56;
 Matches 317; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 956 CTAGGCCACAATAATTACGGCTCTGTGATTTACGATTTTACTGCAATTTTTCGAT 1015
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 Db 323 CTAGGCCACAATAATTACGGCTCTGTGATTTACGATTTTACTGCAATTTTTCGAT 264

QY 1016 TGCCTTTTTTTTTGGCCAAACCCCTACTCCGGTAAATATCACTTTCCGTGTGTAC 1075
 |||||||
 Db 263 TGCCTTTTTTTTTGGCCAAACCCCTACTCCGGTAAATATCACTTTCCGTGTGTAC 204

QY 1076 ATTTGTCAAAAACCCCTGAACCCCTACTTTCTGCGGTGCGCTACCGCTCCGCTTC 1135
 |||||||
 Db 203 ATTTGTCAAAAACCCCTGAACCCCTACTTTCTGCGGTGCGCTACCGCTCCGCTTC 144

QY 1136 TTCCACATTTCCAAAGTACCCCTGATCTCATAATATCATCTTCACTTACTGCTCTT 1195
 |||||||
 Db 143 TTCCACATTTCCAAAGTACCCCTGATCTCATAATATCATCTTCACTTACTGCTCTT 84

QY 1196 TTGCGTGGCTCTTCCAACTCCGCCAAATTCCTGTACGGGTACGCACTTTGATTTA 1255
 |||||||
 Db 83 TTGCGTGGCTCTTCCAACTCCGCCAAATTCCTGTACGGGTACGCACTTTGATTTA 24

QY 1256 TTTTTCCAATTTGTTTCTCTC 1278
 |||||||
 Db 23 TTTTTCCAATTTGTTTCTCTC 1

RESULT 5
 AV181369/c 300 bp mRNA linear EST 21-JUL-1999
 LOCUS AV181369 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
 DEFINITION embryo Caenorhabditis elegans cDNA clone yk619e10 3', mRNA
 sequence.
 ACCESSION AV181369
 VERSION AV181369.1 GI:5561270
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Pelodierinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 300)
 AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
 Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
 M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
 Nomoto,H.
 TITLE Expressed genes in C.elegans
 JOURNAL Unpublished (1999)
 COMMENT Contact: Yuji Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: yk@haraelab.nig.ac.jp.
 FEATURES
 source location/Qualifiers
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 /organism="Caenorhabditis elegans"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone="yk619e10"
 /clone_lib="Yuji Kohara unpublished cDNA:Strain N2
 hermaphrodite embryo"
 /sex="hermaphrodite"
 /dev_stage="embryo"

BASE COUNT 103 a 44 c 90 g 62 t 1 others
 ORIGIN

Query Match 22.7%; Score 299; DB 9; Length 300;
 Best Local Similarity 99.7%; Pred. No. 1.2e-52;
 Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 944 GAAGTGGGAAGCTAGGACCAAAATTTACGGCTCTGTGTCGATTTACGATTTTACTGCA 1003
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 Db 300 GAAGTGGGAAGCTAGGACCAAAATTTACGGCTCTGTGTCGATTTACGATTTTACTGCA 241

QY 1004 ATTTTTCGATGCTTTTGTGGCCAAACCTACTTCGCTAATATCACTTTC 1063
 DB 240 ATTTTTCGATGCTTTTGTGGCCAAACCTACTTCGCTAATATCACTTTC 181
 QY 1064 CGGTGCTGATATTCGCAAAACCCGAAACCTAATCTTTCGCGGTGCTAGC 1123
 DB 180 CGGTGCTGATATTCGCAAAACCCGAAACCTAATCTTTCGCGGTGCTAGC 121
 QY 1124 CTCGCCCTCTCTTCACATTTCCAAAGTACCCCTGATCTCAATATTCATCTTCACTT 1183
 DB 120 CTCGCCCTCTCTTCACATTTCCAAAGTACCCCTGATCTCAATATTCATCTTCACTT 61
 QY 1184 TAACTGTCTTTTGTGTGGGCTCTTCCACTCCCCCAATTCCTAGCGTACGCG 1243
 DB 60 TAACTGTCTTTTGTGTGGGCTCTTCCAACTCCCCCAATTCCTGATACGCGTACGCG 1
 RESULT 6
 LOCUS AV191206 360 bp mRNA linear EST 22-JUL-1999
 DEFINITION AV191206 Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo *Caenorhabditis elegans* cDNA clone yk591c12 5', mRNA sequence.
 ACCESSION AV191206.1 GI:5573358
 VERSION AV191206
 KEYWORDS EST.
 SOURCE *Caenorhabditis elegans*.
 ORGANISM *Caenorhabditis elegans*.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea; Rhabditidae; Pelodertinae; *Caenorhabditis*.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H., Nishigaki, A., Motohashi, T., Deng, Q., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A., Mitani, Y., Iida, K., Oesugi, H., Sugiyama, Y. and Nomoto, H.
 COMMENT Expressed genes in *C. elegans*
 TITLE Unpublished (1999)
 JOURNAL Contact: Yui Kohara
 COMMENT Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykoha@elab.nig.ac.jp.
 FEATURES
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 Location/Qualifiers
 /organism="Caenorhabditis elegans"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone="yk591c12"
 /clone_1lb="Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo"
 /sex="hermaphrodite"
 /dev_stage="embryo"
 BASE COUNT 110 a 77 c 93 g 74 t 6 others
 ORIGIN
 Query Match 22.5% Score 295.6; DB 9; Length 360;
 Best Local Similarity 90.0% Pred. No. 5.6e-57;
 Matches 324; Conservative 0; Mismatches 35; Indels 1; Gaps 1;
 QY 45 GCGGATCGGCGGCAAGATGCGACTGGGAGATGAAGAGTTTCTGGGGATAAAGG 104
 DB 1 GCGGATCGGCGGCAAGATGCGACTGGGAGATGAAGAGTTTCTGGGGATAAAGG 60
 QY 105 CACAGAGCCACCGATTTTGAATCAATAGTAGTCTAGAGACTTGGCATACCGAGTAG 164
 DB 61 CACAGAGCCACCGATTTTGAATCAATAGTAGTCTAGAGACTTGGCATACCGAGTAG 120
 QY 165 GAGGCTTGAGAGCGAAGATGTCATGAGAGTCAATGTGGAAGAAATCAATGATG 224
 DB 121 GAGGCTTGAGAGCGAAGATGTCATGAGAGTCAATGTGGAAGAAATCAATGATG 180

QY 225 GGAAGACCCAGGCTTGATATCGAGGATTTGTGTCGACTATTTCACGACCGAATCCG 284
 DB 181 GGAAGACCCAGGCTTGATATCGAGGATTTGTGTCGACTATTTCACGACCGAATCCG 240
 QY 285 GCAAAACGGAATGGAATGTTTGGAGACCGGATTTGCCGTGGAGTGAACCGGAGCA 344
 DB 241 GCAAAACGGAATGGAATGTTTGGAGACCGGATTTGCCGTGGAGTGAACCGGAGCA 299
 QY 345 CGAATGATCGAGTATGGAACGATATTTGAGAAAGACGCGGAAATTTTGAAGC 404
 DB 300 CGAATGATCGAGTATGGAACGATATTTGAGAAAGACGCGGAAATTTTGAAGC 359
 RESULT 7
 LOCUS C39078/c 300 bp mRNA linear EST 18-OCT-1999
 DEFINITION C39078 Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo *Caenorhabditis elegans* cDNA clone yk503f3 3', mRNA sequence.
 ACCESSION C39078.1 GI:2375315
 VERSION C39078
 KEYWORDS EST.
 SOURCE *Caenorhabditis elegans*.
 ORGANISM *Caenorhabditis elegans*.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea; Rhabditidae; Pelodertinae; *Caenorhabditis*.
 REFERENCE 1 (bases 1 to 300)
 AUTHORS Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A. and Nishigaki, A.
 COMMENT Expression map of the *C. elegans* genome
 TITLE Unpublished (1996)
 JOURNAL Contact: Yui Kohara
 COMMENT Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykoha@elab.nig.ac.jp.
 FEATURES
 source
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 Location/Qualifiers
 /organism="Caenorhabditis elegans"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone="yk503f3"
 /clone_1lb="Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo"
 /sex="hermaphrodite"
 /dev_stage="embryo"
 BASE COUNT 111 a 43 c 68 g 64 t 14 others
 ORIGIN
 Query Match 21.3% Score 279.6; DB 14; Length 300;
 Best Local Similarity 94.0% Pred. No. 1.4e-48;
 Matches 282; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 QY 918 TGAATTCATCAATCTTGAAGTGAAGAGTGGAAAGCTAGGCCAACAATAGGCTCT 977
 DB 300 TGAATTCATCAATCTTGAAGTGAAGAGTGGAAAGTGGAAAGTGGAAATAGGCTCT 241
 QY 978 CTGTGTCGATTTACGATTTTACTGCAATTTTTCGATGCTTTTGTGGCCAAAC 1037
 DB 240 CTGTGTCGATTTACGATTTTANTGCAATTTTTCGATGCTTTTGTGGCCAAAC 181
 QY 1038 CTACTTCGCGGTAAATCAACTTTTCGCGTCTGTACATTTGTCGAAAAACCTGAAAC 1097
 DB 180 CTACTTCGCGGTAAATCAACTTTTCGCGTCTGTACATTTGTCGAAAAACCTGAAAC 121
 QY 1098 CTTAATCTTCTCGCGGTGCGCTAGCCTCCGCTCTCTTCCACATTTCCAAAGTACCC 1157
 DB 120 CTTAATCTTCTCGCGGTGCGCTAGCCTCCGCTCTCTTCCACATTTCCAAAGTACCC 61
 QY 1158 TGTATCTCAATTAATCTTCACTTAACTGTCCTTTTGTGCTGCTTCCCAATC 1217

Db 60 TGTATCTCAATTAATTCATTACCTTAACTGTCTTTTNGTGGCCCTTCCAACTC 1

RESULT 8 300 bp mRNA linear EST 18-OCT-1999
C31912/c C31912

LOCUS C31912

DEFINITION C31912 Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo

ACCESSION C31912

VERSION C31912.1 GI:2363708

KEYWORDS EST.

SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans.

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea / Rhabditidae; Peloderae; Caenorhabditis.

AUTHORS Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A. and Nishigaki, A.

TITLE Expression map of the C.elegans genome

JOURNAL Unpublished (1996)

COMMENT Contact: Yui Kohara
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Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source 1..300
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_1ib="Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"

BASE COUNT 105 a 44 c 80 g 64 t 7 others

ORIGIN

Query Match 21.0%; Score 275.6; DB 14; Length 300;
Best Local Similarity 96.0%; Pred. No. 9.7e-48;
Matches 289; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 942 AAGAAGTGGGAAGCTAGGCCACAAATTCAGGCTCTGTGCGATTGATTCAGATTTTACG 1001
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Db 300 AAGAAGTGGGAAG-TAGGCCACAAATTCAGGCTCTGTGCGATTGATTCAGATTTTACG 242
QY 1002 CAATTTTTCGATGCTTTTTCGCAACCCCTGATCTTTCGCGGTAATTCACATTT 1061
|||||
Db 241 CAATTTTTCGATGCTTTTTCGCAACCCCTGATCTTTCGCGGTAATTCACATTT 182
QY 1062 TCCGCTTGTGATCAATTCGCAAAACCCCTGAAACCCCTGATCTTTCGCGGTAATTCACATTT 1121
|||||
Db 181 TCCGCTTGTGATCAATTCGCAAAACCCCTGAAACCCCTGATCTTTCGCGGTAATTCACATTT 122
QY 1122 GCGTCCCGCTTCTTCACATTCGCAAAAGTACCCCTGATCTTTCGCGGTAATTCACATTT 1181
|||||
Db 121 GCGTCCCGCTTCTTCACATTCGCAAAAGTACCCCTGATCTTTCGCGGTAATTCACATTT 62
QY 1182 TTTAACTGTCTTTCGCTGTGCGCTTTCACAACTCCCAAAATTCCTGACGGTACG 1241
|||||
Db 61 TTTAACTGTCTTTCGCTGTGCGCTTTCACAACTCCCAAAATTCCTGACGGTACG 2
QY 1242 C 1242
Db 1 C 1

RESULT 9 300 bp mRNA linear EST 18-OCT-1999
C29364/c C29364

LOCUS C29364

DEFINITION C29364 Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo

ACCESSION Caenorhabditis elegans cDNA clone yk201b10 3', mRNA sequence.
C29364
C29364.1 GI:261160

VERSION EST.

KEYWORDS Caenorhabditis elegans.

SOURCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea / Rhabditidae; Peloderae; Caenorhabditis.

ORGANISM Caenorhabditis elegans.

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea / Rhabditidae; Peloderae; Caenorhabditis.

AUTHORS Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A. and Nishigaki, A.

TITLE Expression map of the C.elegans genome

JOURNAL Unpublished (1996)

COMMENT Contact: Yui Kohara
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National Institute of Genetics
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Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source 1..300
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_1ib="Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"

BASE COUNT 105 a 44 c 74 g 63 t 14 others

ORIGIN

Query Match 20.5%; Score 269.2; DB 14; Length 300;
Best Local Similarity 94.0%; Pred. No. 2.1e-46;
Matches 282; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 940 GGAAGAGTGGGAAGCTAGGCCACAAATTCAGGCTCTGTGCGATTGATTCAGATTTTAC 999
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Db 300 GGAAGAGTGGGAAGGAGTGGGCCACAAATTCAGGCTCTGTGCGATTGATTCAGATTTTAC 241
QY 1000 TGCAATTTTTCGATGCTTTTTCGCAACCCCTGATCTTTCGCGGTAATTCACATTT 1059
|||||
Db 240 TGCAATTTTTCGATGCTTTTTCGCAACCCCTGATCTTTCGCGGTAATTCACATTT 181
QY 1060 TTTCCGCTTGTGATCAATTCGCAAAACCCCTGAAACCCCTGATCTTTCGCGGTAATTCACATTT 1118
|||||
Db 180 TTTCCGCTTGTGATCAATTCGCAAAACCCCTGAAACCCCTGATCTTTCGCGGTAATTCACATTT 121
QY 1119 CTAGCTCCCGCTTCTGTGCGCTTTCACAAAGTACCCCTGATCTTTCGCGGTAATTCACATTT 1178
|||||
Db 120 CTAGCTCCCGCTTCTGTGCGCTTTCACAAAGTACCCCTGATCTTTCGCGGTAATTCACATTT 61
QY 1179 CACTTAACTGTCTTTCGCTGTGCGCTTTCACAACTCCCAAAATTCCTGACGGTACG 1238
|||||
Db 60 CACTTAACTGTCTTTCGCTGTGCGCTTTCACAACTCCCAAAATTCCTGACGGTACG 1
QY 1238 C 1238
Db 1 C 1

RESULT 10 360 bp mRNA linear EST 22-JUL-1999
AV193616/c AV193616

LOCUS AV193616

DEFINITION AV193616 Yui Kohara unpublished cDNA:Strain N2 hermaphrodite embryo

ACCESSION Caenorhabditis elegans cDNA clone yk619e10 5', mRNA sequence.
AV193616
AV193616.1 GI:5575768

VERSION EST.

KEYWORDS Caenorhabditis elegans.

SOURCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea / Rhabditidae; Peloderae; Caenorhabditis.

ORGANISM Caenorhabditis elegans.

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea / Rhabditidae; Peloderae; Caenorhabditis.

AUTHORS Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H.,

Nishigaki, A., Motohashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and Nomoto, H.
 Expressed genes in *C.elegans*
 Unpublished (1999)
 Contact: Yuji Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp

FEATURES
 source
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 /organism="Caenorhabditis elegans"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone_lib="Yuji Kohara unpublished cDNA:Strain N2
 hermaprodite embryo"
 /sex="hermaprodite"
 /dev_stage="embryo"

BASE COUNT 104 a 64 c 104 g 84 t 4 others
 ORIGIN

Query Match 19.8%; Score 261; DB 9; Length 360;
 Best Local Similarity 93.8%; Pred. No. 1e-44;
 Matches 303; Conservative 0; Mismatches 17; Indels 3; Gaps 3;

OY 88 TTTCCTGGGATTAAGGACAG-AGCCACCGATTTTGAATCATATGATGCTCAGGA 146
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 Db 38 TTCTGGGGATTAAGGACAGAGCCACCGATTTTGAATCATATGATGCTCAGGA 97
 OY 147 CTTCCCATCACCGAGTAGCGGCTTGAGCGGAGATGCTCGAGAGTCATTTGA 206
 |||
 Db 98 CTTCCCATCACCGAGTAGCGGCTTGAGCGGAGATGCTCGAGAGTCATTTGA 157
 OY 207 TGGAAAAATCATATGTTGGGAAGAGCCAGGCTTGATATCGAGGATTTGTGCTGACTA 266
 |||
 Db 158 TGGAAAAATCATATGTTGGGAAGAGCCAGGCTTGATATCGAGGATTTGTGCTGACTA 217
 OY 267 TTTACGACCGAGATCCGGCAAAACGGAATGATGTTGGACACCGGATTTGCCGTG 326
 |||
 Db 218 TTTACGACCGAGATCCGGCAAAACGGAATGATGTTGGACACCGGATTTGCCGTG 277
 OY 327 TGGAGTGCACCGGACGACGAATGATGCGAGTTATGGAACGATATTCGAG-AAGAGC 385
 |||
 Db 278 TGGAGTGCACCTTTTGTGTTGATGCGAGTTATGGAACGATATTCGAGAAAGAAC 337
 OY 386 ACGC-GGAAAAATTTGAGACCTT 407
 |||
 Db 338 ACGCNGGAAAAATTTGAGACCTT 360

RESULT 11
 AV179317/c 300 bp mRNA linear EST 21-JUL-1999
 LOCUS AV179317 Yuji Kohara unpublished cDNA:Strain N2 hermaprodite
 DEFINITION embryo *Caenorhabditis elegans* cDNA clone yk591c12 3', mRNA
 sequence.
 AV179317
 AV179317.1 GI:5559218
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabdiloidea
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabdiloidea
 1 (bases 1 to 300)
 Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H.,
 Nishigaki, A., Motohashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano,
 M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and
 Nomoto, H.

TITLE
 Expressed genes in *C.elegans*

JOURNAL
 COMMENT
 Unpublished (1999)
 Contact: Yuji Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp

FEATURES
 source
 1.300
 /organism="Caenorhabditis elegans"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone_lib="Yuji Kohara unpublished cDNA:Strain N2
 hermaprodite embryo"
 /sex="hermaprodite"
 /dev_stage="embryo"

BASE COUNT 106 a 42 c 80 g 63 t 9 others
 ORIGIN

Query Match 19.7%; Score 259.4; DB 9; Length 300;
 Best Local Similarity 95.0%; Pred. No. 2.4e-44;
 Matches 285; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

OY 945 AAGTGGAAAGCTAGGCGCAAAATTAACGCTCTGCTGATTTAGCATTTTACTGCA 1004
 |||
 Db 300 AAGTGGAAAGCTAGGCGCAAAATTAACGCTCTGCTGATTTAGCATTTTANTGCA 241
 OY 1005 TTTTTCGATTTGCTTTTGTGCGCAAAACCTTACTTCCGCGGATATCACTTTCC 1064
 |||
 Db 240 TTTTTCGATTTGCTTTTGTGCGCAAAACCTTACTTCCGCGGATATCACTTTCC 181
 OY 1065 GGTCTGTACATTTGCTAATAAACCTTGAACCTTACTTCCGCGGATATCACTTTCC 1124
 |||
 Db 180 GGTCTGTACATTTGCTAATAAACCTTGAACCTTACTTCCGCGGATATCACTTTCC 121
 OY 1125 TCCCGCTCTCTCCATTTCCAAAGTACCCCTGATCTCAATATTCATCTTCACTTT 1184
 |||
 Db 120 TCCCGCTCTCTCCATTTCCAAAGTACCCCTGATCTCAATATTCATCTTCACTTT 61
 OY 1185 AACTGTCTCTTTGCTGCTGCTCTT-CCACTCCCCCAATT-CCGTAGCGGTAGCC 1242
 |||
 Db 60 AACTGTCTCTTTGCTGCTGCTCTT-CCACTCCCCCAATT-CCGTAGCGGTAGCC 1

RESULT 12
 CDS0106X/c 1101 bp DNA linear GSS 26-JUL-1999
 LOCUS CDS0106X20 of Drosophila melanogaster genome survey sequence T7 end of BAC
 DEFINITION BAC03K20 of Drosophila melanogaster genome survey sequence.
 fly), genomic survey sequence.
 AL098595
 AL098595.1 GI:5610206
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
 Pterygota; Drosophila; Drosophila; Drosophila.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Genoscope.
 Direct Submission
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
 http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billard at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector

[illegible]

LOCUS	CNCN0182P	1101 bp	DNA	linear	GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence SP6 end of BAC ACN37D10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL108811				
VERSION	ALI08811.1	GI:5629125			
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster.				
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Empidoidea; Drosophilidae; Drosophila. 1 (bases 1 to 1101)				
REFERENCE	Genoscope. Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr) - Web : www.genoscope.cns.fr)				
AUTHORS	Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.edl.ac.uk -. This drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CERN (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelovBAC11.				
JOURNAL					
COMMENT					
FEATURES	location/Qualifiers				
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BASE COUNT	274 a	268 c	128 g	73 t	358 others
ORIGIN					
Query Match	4.3%; Score 56.6; DB 17; Length 1101;				
Best Local Similarity	20.4%; Pred. No. 0.044;				
Matches	95;	Conservative	188;	Mismatches	179; Indels Gaps 1.
Dn	849	ASCATGAATTTGTGTAATTAAATAAATTAATGATAGTACAAGCTTCATCAATGGATCGATC	908	:: :::::	:: :::::
Dn	1101	WNYNNHNMNTNMADMMHNCHMNUUMIMYUUNHCNUMAHNVMTNGAYAMNHANH	1042	:: :::::	:: :::::
Dn	909	TTKSCATGACTGCSTGCATCCSTTGTCAGTAGCAGAAGTGGGAAGTGGCAAAT	968	:: :::::	:: :::::
Dn	1041	UTWTGTMWTSOMYGUAATGCTGCGNNHMIMMAKAWMMWMYUAMMNINHNMISCMIMH	982	:: :::::	:: :::::
Dn	969	TASSGATCTGTGTCGATTTAGCAATTTAGTCGAAATTTTTCSGATGSGCTTTT	1028	:: :::::	:: :::::
Dn	981	YMNMSCSMSCSMNNHMCNMHNATGMTHNYTUUYVMVGNHTMTMYUUNVMYNHNA	922	:: :::::	:: :::::
Dn	1029	GGSCAAAGCTATCCSGGSGTAATAGTCAAGCTTTCCSGTCCGCTGTCATCTGCAAAA-	1087	:: :::::	:: :::::
Dn	921	AMADAAMHAANTNWUANAHANNITUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU	862	:: :::::	:: :::::
Dn	1088	--AASGTAAAGCTATCTTCTGTCGSSGCTGCCGAGTCCGAGTCCGCTGTCGCAATT	1145	:: :::::	:: :::::
Dn	861	WTAINNNHHNNHYMAATTTTTTTTTTTTTTWNNHHNNHTUUUUUUUUUUUUUUUUUU	802	:: :::::	:: :::::
Dn	1146	CSAAGTACCSTGATATGTAATATGATATGATGATGATGATGATGATGATGATGATG	1205	:: :::::	:: :::::
Dn	801	WYUUUAUUGUCSNATHNYMUUUSTUUMIHANAATMTATMTATMTATMTATMTATMT	742	:: :::::	:: :::::
Dn	1206	CTGTTCGCAAGTCCCCAAATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	1265	:: :::::	:: :::::
Dn	741	MTWTATMTSCNHCNMCHMMIMMCTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTU	682	:: :::::	:: :::::
Dn	1266	ATTGTTTCTCTCACACAAAAAAAOOGTCAAAAAAA	1310	:: :::::	:: :::::
Dn	681	YCUCGYWNTHTTTCGCHNTTMSCAMGSCSTTTTTTAAAMA	637	:: :::::	:: :::::

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